

78225

RECEIVED SEARCH REQUEST FORM

Access DB# _____

OCT 21 2002 Scientific and Technical Information Center

Requester's Full Name: John W. Lin Examiner #: 69507 Date: 10-21-02
 Art Unit: 1646 Phone Number 303-4008 Serial Number: 09/838028
 Mail Box and Bldg/Room Location: CM1 10D19 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEO IP NO! 2 of
 09/838028. (two)

10D19

Point of Contact:
 Beverly Shears
 Technical Info. Specialist
 CM1 1E05 Tel: 308-4994

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: Beverly 4994 NA Sequence (#) _____ STN _____
 Searcher Phone #: _____ AA Sequence (#) _____ Dialog _____
 Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: _____ Bibliographic _____ Dr. Link _____
 Date Completed: 10-22-02 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: 3 Fulltext _____ Sequence Systems _____
 Clerical Prep Time: _____ Patent Family _____ WWW/Internet _____
 Online Time: 20 Other _____ Other (specify) CGN

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Tue Oct 22 10:58:57 2002

us-09-838-028-2.rapm

Ulm
09/838028 Page 1
Seq. ID 2 w/Interf

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:45 : Search time 113 Seconds
(without alignments)
1404.807 Million cell updates/sec

Title: US-09-838-028-2
Perfect score: 2318
Sequence: 1 MESSPIRQSSGNSSTLGRVP.....SDIIMSDSYLRPASPRLS 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues
Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending-Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2318	100.0	451	1 PCT-US01-10436-3	Sequence 3, Appli
2	2318	100.0	451	19 US-09-533-687-2	Sequence 3, Appli
3	2318	100.0	451	21 US-09-714-008A-12	Sequence 12, Appli
4	2318	100.0	451	21 US-09-740-0033-2	Sequence 2, Appli
5	2318	100.0	451	21 US-09-815-499-2	Sequence 2, Appli
6	2318	100.0	451	22 US-09-838-028-2	Sequence 2, Appli
7	2318	100.0	451	22 US-09-860-797-2	Sequence 2, Appli

8	2318	100.0	451	22	US-09-864-029-22	Sequence 22, Appli
9	2318	100.0	451	23	US-09-980-049-3	Sequence 3, Appli
10	2318	100.0	451	24	US-09-995-543-12	Sequence 12, Appli
11	2318	100.0	451	23	US-10-096-511-12	Sequence 12, Appli
12	2318	100.0	451	26	US-60-202-278-1	Sequence 1, Appli
13	2318	100.0	451	26	US-60-317-661-2	Sequence 2, Appli
14	2318	100.0	451	26	US-60-329-926-2	Sequence 2, Appli
15	2318	100.0	869	23	US-09-714-008A-84	Sequence 100, App
16	2318	100.0	869	23	US-09-995-543-100	Sequence 100, App
17	2318	100.0	869	24	US-10-096-511-100	Sequence 100, App
18	2317	100.0	451	22	US-09-864-029-24	Sequence 24, Appli
19	2313	99.8	451	21	US-09-714-008A-84	Sequence 84, Appli
20	2313	99.8	451	23	US-09-995-543-84	Sequence 84, Appli
21	2313	99.8	451	24	US-10-096-511-84	Sequence 84, Appli
22	2219	95.7	529	26	US-60-212-655-705	Sequence 705, App
23	2219	95.7	529	26	US-60-229-515-939	Sequence 939, App
24	2219	95.7	555	26	US-60-212-655-407	Sequence 407, App
25	2219	95.7	555	26	US-60-229-515-974	Sequence 974, App
26	2219	95.7	672	26	US-60-329-515-1243	Sequence 1243, Ap
27	2204	95.1	449	22	US-09-838-028-4	Sequence 4, Appli
28	2106	90.9	417	26	US-60-317-661-11	Sequence 11, Appli
29	2106	90.9	417	26	US-60-329-926-11	Sequence 11, Appli
30	1276	55.0	252	9	US-08-513-974-52	Sequence 52, Appli
31	1276	55.0	252	18	US-09-461-436-52	Sequence 360, App
32	1276	55.0	252	18	US-09-461-436-360	Sequence 1253, Ap
33	1276	55.0	252	22	US-09-864-029-36	Sequence 263, App
34	1162	50.1	221	26	US-60-192-587-1253	Sequence 1254, Ap
35	999.5	43.1	196	26	US-60-186-281-263	Sequence 221, App
36	999.5	43.1	201	26	US-60-192-738-306	Sequence 306, App
37	999.5	43.1	201	26	US-60-194-114-221	Sequence 221, App
38	982	42.8	187	26	US-60-192-587-1254	Sequence 1254, Ap
39	897	38.3	169	26	US-60-196-713-2476	Sequence 2476, Ap
40	823	35.5	422	22	US-09-864-029-37	Sequence 37, Appli
41	823	35.5	428	26	US-60-317-661-12	Sequence 12, Appli
42	823	35.5	428	26	US-60-329-926-12	Sequence 12, Appli
43	821.5	35.4	419	21	US-09-740-0033-4	Sequence 4, Appli
44	790.5	34.1	160	26	US-60-192-587-1124	Sequence 1124, Ap
45	790.5	34.1	160	26	US-60-194-091-1107	Sequence 1107, Ap

ALIGNMENTS

RESULT 1
PCT-US01-10436-3
: Sequence 3, Application PCT/US0110436
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: POLICKY, Jennifer L.
: APPLICANT: TRIBOULEY, Catherine M.
: APPLICANT: TANG, Y. Tom
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: GRAUL, Richard
: APPLICANT: KHAN, Farrah A.
: APPLICANT: NGUYEN, Daniel B.
: APPLICANT: PATTERSON, Chandra
: APPLICANT: LAL, Preeti
: APPLICANT: AU-YOUNG, Janice
: APPLICANT: YANG, Junming
: APPLICANT: HAFALIA, April
: APPLICANT: WALIA, Narinder K.
: APPLICANT: DAS, Debopriya
: TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
: FILE REFERENCE: PI-0072 PCT
: CURRENT FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: PCT/US01/10436
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: 60/193,051
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/199,084
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: 60/200,551

;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: 60/202,278
;; PRIOR FILING DATE: 2000-05-05
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PERL Program
;; SEQ ID NO 3
;; LENGTH: 451
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No: 3226980CD1
PCT-US01-10436-3

Query Match 100.0%; Score 2318; DB 1; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.3e-207;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AAVNAVIKTPALKRKFVFFVHLCVLDLAALTLPPLAMSSALFDHALFGEVACRLYLF 120
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DB 121 LSVCFVSLATLSVSAINVERIYVYVHPKRYEVRMTGLVASVLGVWVKALAMASVPLG 180
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DB 181 RVSMEEGAPVPPGCSLQWHSAYCOLFVVFAVLYFLPLLLILVYCSMFVAVARAAM 240
QY 241 QHGFLPTMETPRQSGESLSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGQFLLCW 300
DB 241 QHGFLPTMETPRQSGESLSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGQFLLCW 300
QY 301 LPYFSFHLVYALSAQPISTGQVESVTWIGYFCFTSNPFYGCINROIKRELKQFVCF 360
DB 301 LPYFSFHLVYALSAQPISTGQVESVTWIGYFCFTSNPFYGCINROIKRELKQFVCF 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSESWSRPLSPKQEPVAVDFRIPOGIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSESWSRPLSPKQEPVAVDFRIPOGIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 2

US-09-533-687-2

;; Sequence 2, Application US/09533687
;; GENERAL INFORMATION:
;; APPLICANT: Usman Shadon
;; APPLICANT: Mahanandeeswar Gattu
;; APPLICANT: David Michaelovich
;; APPLICANT: Nabih Elshourbagy
;; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR
;; TITLE OF INVENTION: (AXOR64)
;; FILE REFERENCE: GP-70684
;; CURRENT APPLICATION NUMBER: US/09/533.687
;; CURRENT FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 451
;; TYPE: PRT
;; ORGANISM: HOMO SAPIENS
US-09-533-687-2

Query Match 100.0%; Score 2318; DB 19; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.3e-207;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
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DB 61 AAVNAVIKTPALKRKFVFFVHLCVLDLAALTLPPLAMSSALFDHALFGEVACRLYLF 120
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QY 181 RVSMEEGAPVPPGCSLQWHSAYCOLFVVFAVLYFLPLLLILVYCSMFVAVARAAM 240
DB 181 RVSMEEGAPVPPGCSLQWHSAYCOLFVVFAVLYFLPLLLILVYCSMFVAVARAAM 240
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DB 241 QHGFLPTMETPRQSGESLSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGQFLLCW 300
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DB 301 LPYFSFHLVYALSAQPISTGQVESVTWIGYFCFTSNPFYGCINROIKRELKQFVCF 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSESWSRPLSPKQEPVAVDFRIPOGIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSESWSRPLSPKQEPVAVDFRIPOGIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 3

US-09-714-008A-12

;; Sequence 12, Application US/09714008A
;; GENERAL INFORMATION:
;; APPLICANT: Dang, Rupong
;; APPLICANT: Lowitz, Kevin P.
;; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled Receptors
;; FILE REFERENCE: AREN0086
;; CURRENT APPLICATION NUMBER: US/09/714,008A
;; CURRENT FILING DATE: 2000-11-16
;; Prior application data removed - consult PAM or file wrapper
;; NUMBER OF SEQ ID NOS: 133
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 12
;; LENGTH: 451
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-714-008A-12

Query Match 100.0%; Score 2318; DB 21; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.3e-207;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAVNAVIKTPALKRKFVFFVHLCVLDLAALTLPPLAMSSALFDHALFGEVACRLYLF 120
DB 61 AAVNAVIKTPALKRKFVFFVHLCVLDLAALTLPPLAMSSALFDHALFGEVACRLYLF 120
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DB 121 LSVCFVSLATLSVSAINVERIYVYVHPKRYEVRMTGLVASVLGVWVKALAMASVPLG 180

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Db 181 RVSMEGAPSVPGCSLQMSHSAVCQLFVVYFAVLVFLPLLILVYCSMFRAVARAAM 240
Qy 241 OHGPLPTMETPRORSELSRSSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
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Qy 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 4
US-09-740-033-2

; Sequence 2, Application US/09740033
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001056
; CURRENT APPLICATION NUMBER: US/09/740.033
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Human
; US-09-740-033-2

Query Match 100.0%; Score 2318; DB 21; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 LSVCFVSLALISVAINERYYYVHPMKRYEVRMTGLIVASVLYGVWVKALAMASVPLG 180
Qy 181 RVSMEGAPSVPGCSLQMSHSAVCQLFVVYFAVLVFLPLLILVYCSMFRAVARAAM 240
Db 181 RVSMEGAPSVPGCSLQMSHSAVCQLFVVYFAVLVFLPLLILVYCSMFRAVARAAM 240
Qy 241 OHGPLPTMETPRORSELSRSSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
Db 241 OHGPLPTMETPRORSELSRSSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
Qy 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROIRGELSKQVCFE 360
Db 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROIRGELSKQVCFE 360
Qy 361 KPAPEEELRLPSRGSIENFLQLOGTGCPSSESVSRPLSPKQEPYAVDFRIPGOIAE 420
Db 361 KPAPEEELRLPSRGSIENFLQLOGTGCPSSESVSRPLSPKQEPYAVDFRIPGOIAE 420
Qy 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451

Db 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 5
US-09-815-499-2

; Sequence 2, Application US/09815499
; GENERAL INFORMATION:
; APPLICANT: Elshoubagy, Nabli
; APPLICANT: Gattu, Mahanandeshwar
; APPLICANT: Michalovich, David
; TITLE OF INVENTION: Molecular Cloning of a 7Tm Receptor (AX0864)
; FILE REFERENCE: GB70684-1
; CURRENT APPLICATION NUMBER: US/09/815.499
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 09/533,667
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: GB 0027166.8
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-815-499-2

Query Match 100.0%; Score 2318; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MESSPIPOSSGNSSTLGVNTPQTPGASTAGVPEVGLRDVASESVALFFMLLLDITAVAGN 60
Qy 61 AAVNAVIKTPALRKRFVVFHLCIVDLALTLPLMLSSSALFDHALFGEVACRYLTF 120
Db 61 AAVNAVIKTPALRKRFVVFHLCIVDLALTLPLMLSSSALFDHALFGEVACRYLTF 120
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Db 121 LSVCFVSLALISVAINERYYYVHPMKRYEVRMTGLIVASVLYGVWVKALAMASVPLG 180
Qy 181 RVSMEGAPSVPGCSLQMSHSAVCQLFVVYFAVLVFLPLLILVYCSMFRAVARAAM 240
Db 181 RVSMEGAPSVPGCSLQMSHSAVCQLFVVYFAVLVFLPLLILVYCSMFRAVARAAM 240
Qy 241 OHGPLPTMETPRORSELSRSSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
Db 241 OHGPLPTMETPRORSELSRSSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
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Db 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROIRGELSKQVCFE 360
Qy 361 KPAPEEELRLPSRGSIENFLQLOGTGCPSSESVSRPLSPKQEPYAVDFRIPGOIAE 420
Db 361 KPAPEEELRLPSRGSIENFLQLOGTGCPSSESVSRPLSPKQEPYAVDFRIPGOIAE 420
Qy 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 6
US-09-838-028-2

; Sequence 2, Application US/09838028
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Berthold, Malin
; TITLE OF INVENTION: Novel G Protein-Coupled Receptor
; FILE REFERENCE: 00125US2

```
; CURRENT APPLICATION NUMBER: US/09/838,028
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/198,600
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-838-028-2

Query Match          100.0%; Score 2318; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEGLRDVASESVALPFMLLDLTAAVAGN 60
    |||||||
DB 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEGLRDVASESVALPFMLLDLTAAVAGN 60
QY 61 AAVNAVIKTPALKRKFEVFHFLCLVDLLAALTLPMLAMSSSALFDHALFGEVACRLYLF 120
    |||||||
DB 61 AAVNAVIKTPALKRKFEVFHFLCLVDLLAALTLPMLAMSSSALFDHALFGEVACRLYLF 120
QY 121 LSVCFVSLATLSVAINVERYYYVHPRKYEVRMTGLVASVLGVVWKALAMASVPLG 180
    |||||||
DB 121 LSVCFVSLATLSVAINVERYYYVHPRKYEVRMTGLVASVLGVVWKALAMASVPLG 180
QY 181 RVSNEEGAPSPVPCGSLQMSHSAYCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
    |||||||
DB 181 RVSNEEGAPSPVPCGSLQMSHSAYCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
QY 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
    |||||||
DB 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
QY 301 LPRYSFHLVYALSAOPISTGVESVVTWIGYFCTSNPFYGCILNROIKGLSKQFCFF 360
    |||||||
DB 301 LPRYSFHLVYALSAOPISTGVESVVTWIGYFCTSNPFYGCILNROIKGLSKQFCFF 360
QY 361 KPAPEEELRLPSREGSIEENLFQGTGCPSESWSRPLSPQOEPPAVDFRIPQIAE 420
    |||||||
DB 361 KPAPEEELRLPSREGSIEENLFQGTGCPSESWSRPLSPQOEPPAVDFRIPQIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 7
US-09-860-797-2
; Sequence 22, Application US/09860797
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Marilyn Evelyn Lewis
; APPLICANT: Nicola Melanle Robas
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PCS10924APME
; CURRENT APPLICATION NUMBER: US/09/860,797
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: GB 0012248.1
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 0107394.9
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/211,421
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/283,441
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-860-797-2

Query Match          100.0%; Score 2318; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEGLRDVASESVALPFMLLDLTAAVAGN 60
    |||||||
DB 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEGLRDVASESVALPFMLLDLTAAVAGN 60
QY 61 AAVNAVIKTPALKRKFEVFHFLCLVDLLAALTLPMLAMSSSALFDHALFGEVACRLYLF 120
    |||||||
DB 61 AAVNAVIKTPALKRKFEVFHFLCLVDLLAALTLPMLAMSSSALFDHALFGEVACRLYLF 120
QY 121 LSVCFVSLATLSVAINVERYYYVHPRKYEVRMTGLVASVLGVVWKALAMASVPLG 180
    |||||||
DB 121 LSVCFVSLATLSVAINVERYYYVHPRKYEVRMTGLVASVLGVVWKALAMASVPLG 180
QY 181 RVSNEEGAPSPVPCGSLQMSHSAYCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
    |||||||
DB 181 RVSNEEGAPSPVPCGSLQMSHSAYCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
QY 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
    |||||||
DB 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
QY 301 LPRYSFHLVYALSAOPISTGVESVVTWIGYFCTSNPFYGCILNROIKGLSKQFCFF 360
    |||||||
DB 301 LPRYSFHLVYALSAOPISTGVESVVTWIGYFCTSNPFYGCILNROIKGLSKQFCFF 360
QY 361 KPAPEEELRLPSREGSIEENLFQGTGCPSESWSRPLSPQOEPPAVDFRIPQIAE 420
    |||||||
DB 361 KPAPEEELRLPSREGSIEENLFQGTGCPSESWSRPLSPQOEPPAVDFRIPQIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 8
US-09-864-029-22
; Sequence 22, Application US/09864029
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchiernev, Velizar T.
; APPLICANT: Grosche, William M.
; APPLICANT: Szekeres Jr., Edward S.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Gangoli, Esha A.
; APPLICANT: MacDougall, John R.
; APPLICANT: Stone, David J.
; APPLICANT: Smitson, Glenda
; TITLE OF INVENTION: NOVEL GPCR-LIKE PROTEINS AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 21402-022
; CURRENT APPLICATION NUMBER: US/09/864,029
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/206,757
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/214,372
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/219,786
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/207,020
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/220,593
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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/239,542
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/256,402
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/271,645
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/274,809
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/275,590
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-029-22
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Query Match          100.0%: Score 2318: DB 22: Length 451:
Best Local Similarity 100.0%: Pred. No. 1.3e-207:
Matches 451: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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QY 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFEMLLDLTAVAGN 60
   |||||||
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFEMLLDLTAVAGN 60

QY 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLSSALFDHALFGEVACRLYLE 120
   |||||||
Db 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLSSALFDHALFGEVACRLYLE 120

QY 121 LSVCFVSLAILSVSAINVERYYVYVHPMYEVRMTGLVASLVGVWYKALMASVPVLG 180
   |||||||
Db 121 LSVCFVSLAILSVSAINVERYYVYVHPMYEVRMTGLVASLVGVWYKALMASVPVLG 180

QY 181 RVSMEGAPSVPGCSLQMSHSAYCOLFEVYVAVLYFLPLLLILVYCSMFRVARVAM 240
   |||||||
Db 181 RVSMEGAPSVPGCSLQMSHSAYCOLFEVYVAVLYFLPLLLILVYCSMFRVARVAM 240

QY 241 QHGPLETWMETPRQSESISSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGOFLLCW 300
   |||||||
Db 241 QHGPLETWMETPRQSESISSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGOFLLCW 300

QY 301 LPEFSHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360
   |||||||
Db 301 LPEFSHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360

QY 361 KPAPEEELRLPREGSIEENFIQFLOGTCGPSESWSRPLPSKQEPRAVDPRIRIGQIAE 420
   |||||||
Db 361 KPAPEEELRLPREGSIEENFIQFLOGTCGPSESWSRPLPSKQEPRAVDPRIRIGQIAE 420

QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
   |||||||
Db 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
```

```

RESULT 9
US-09-980-049-3
; Sequence 3, Application US/09980049
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LAU, Freeth
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HAFALIA, April
```

```

; APPLICANT: WALIA, Narinder K.
; APPLICANT: DAS, Debopriya
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0072 PCT
; CURRENT APPLICATION NUMBER: US/09/980,049
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,2
; PRIOR FILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: 3226980CD1
US-09-980-049-3
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Query Match          100.0%: Score 2318: DB 23: Length 451:
Best Local Similarity 100.0%: Pred. No. 1.3e-207:
Matches 451: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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QY 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFEMLLDLTAVAGN 60
   |||||||
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFEMLLDLTAVAGN 60

QY 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLSSALFDHALFGEVACRLYLE 120
   |||||||
Db 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLSSALFDHALFGEVACRLYLE 120

QY 121 LSVCFVSLAILSVSAINVERYYVYVHPMYEVRMTGLVASLVGVWYKALMASVPVLG 180
   |||||||
Db 121 LSVCFVSLAILSVSAINVERYYVYVHPMYEVRMTGLVASLVGVWYKALMASVPVLG 180

QY 181 RVSMEGAPSVPGCSLQMSHSAYCOLFEVYVAVLYFLPLLLILVYCSMFRVARVAM 240
   |||||||
Db 181 RVSMEGAPSVPGCSLQMSHSAYCOLFEVYVAVLYFLPLLLILVYCSMFRVARVAM 240

QY 241 QHGPLETWMETPRQSESISSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGOFLLCW 300
   |||||||
Db 241 QHGPLETWMETPRQSESISSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGOFLLCW 300

QY 301 LPEFSHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360
   |||||||
Db 301 LPEFSHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360

QY 361 KPAPEEELRLPREGSIEENFIQFLOGTCGPSESWSRPLPSKQEPRAVDPRIRIGQIAE 420
   |||||||
Db 361 KPAPEEELRLPREGSIEENFIQFLOGTCGPSESWSRPLPSKQEPRAVDPRIRIGQIAE 420

QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
   |||||||
Db 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
```

```

RESULT 10
US-09-995-543-12
; Sequence 12, Application US/09995543
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T. T.
; APPLICANT: Lowitz, Kevin P. P.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
; FILE REFERENCE: Aren-0311
; CURRENT APPLICATION NUMBER: US/09/995,543
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/226,760
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/714,008
```


Db 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIGQIAE 420
Qy 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451
Db 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451

RESULT 12

US-60-202-278-1

; Sequence 1, Application US/60202278

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Au-Young, Janice

; APPLICANT: Policky, Jennifer L.

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: PI-0088 P

; CURRENT APPLICATION NUMBER: US/60/202, 278

; CURRENT FILING DATE: 2000-05-05

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PERL Program

; SEQ ID NO 1

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; OTHER INFORMATION: Incyte ID No: 3226980CD1

US-60-202-278-1

Query Match

100.0%; Score 2318; DB 26; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.3e-207;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Qy 61 AAVMAVIAKTPALRKRFVVFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Db 61 AAVMAVIAKTPALRKRFVVFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Qy 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Db 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Qy 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Db 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Qy 181 RVSMEGAPSVPPGCSLQMSHSAYCQLFVVVFAVLFLPLLLILVYCSMFRVARVAM 240
Db 181 RVSMEGAPSVPPGCSLQMSHSAYCQLFVVVFAVLFLPLLLILVYCSMFRVARVAM 240
Qy 241 OHGPIPTMMEPRORSSELSRSTWTSAGAPQTPHRTFGGKAAYVLLAVGGFLLCW 300
Db 241 OHGPIPTMMEPRORSSELSRSTWTSAGAPQTPHRTFGGKAAYVLLAVGGFLLCW 300
Qy 301 LPYFSFHLHYVALSAOPISGTGVESVVTWIGYCFSTSNPFYGCCLNRQIRGELSKEQVCF 360
Db 301 LPYFSFHLHYVALSAOPISGTGVESVVTWIGYCFSTSNPFYGCCLNRQIRGELSKEQVCF 360
Qy 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIGQIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIGQIAE 420
Qy 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451
Db 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451

RESULT 13

US-60-317-661-2

; Sequence 2, Application US/60317661

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,

; TITLE OF INVENTION: HGPBMY32, EXPRESSED HIGHLY IN BRAIN TISSUE

; FILE REFERENCE: D0183 psp
; CURRENT APPLICATION NUMBER: US/60/317, 661
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens

US-60-317-661-2

; Sequence 1, Application US/60329926

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; APPLICANT: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,

; TITLE OF INVENTION: HGPBMY32, EXPRESSED HIGHLY IN BRAIN TISSUE

; FILE REFERENCE: D0183 psp1

; CURRENT APPLICATION NUMBER: US/60/329, 926

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; OTHER INFORMATION: Incyte ID No: 3226980CD1

; OTHER INFORMATION: Incyte ID No: 3226980CD1

; OTHER INFORMATION: Incyte ID No: 3226980CD1

; OTHER INFORMATION: Incyte ID No: 3226980CD1

Query Match

100.0%; Score 2318; DB 26; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.3e-207;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Qy 61 AAVMAVIAKTPALRKRFVVFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Db 61 AAVMAVIAKTPALRKRFVVFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Qy 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Db 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Qy 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Db 121 LSVCFVSLAITSVSAINVERYYVHPMKREYRMTLGLVASYLVGVWVKALAMASVPYLG 180
Qy 181 RVSMEGAPSVPPGCSLQMSHSAYCQLFVVVFAVLFLPLLLILVYCSMFRVARVAM 240
Db 181 RVSMEGAPSVPPGCSLQMSHSAYCQLFVVVFAVLFLPLLLILVYCSMFRVARVAM 240
Qy 241 OHGPIPTMMEPRORSSELSRSTWTSAGAPQTPHRTFGGKAAYVLLAVGGFLLCW 300
Db 241 OHGPIPTMMEPRORSSELSRSTWTSAGAPQTPHRTFGGKAAYVLLAVGGFLLCW 300
Qy 301 LPYFSFHLHYVALSAOPISGTGVESVVTWIGYCFSTSNPFYGCCLNRQIRGELSKEQVCF 360
Db 301 LPYFSFHLHYVALSAOPISGTGVESVVTWIGYCFSTSNPFYGCCLNRQIRGELSKEQVCF 360
Qy 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIGQIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIGQIAE 420
Qy 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451
Db 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451

RESULT 14

US-60-329-926-2

; Sequence 2, Application US/60329926

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,

; TITLE OF INVENTION: HGPBMY32, EXPRESSED HIGHLY IN BRAIN TISSUE

```
Oy 61 AAVMAVIAKTPALRKKEVFEVHFLCLVDLLAALTMLPMLSSSALFDHALFGEVACRLYLE 120
    |||||||
Db 61 AAVMAVIAKTPALRKKEVFEVHFLCLVDLLAALTMLPMLSSSALFDHALFGEVACRLYLE 120
Oy 121 LSVCFVSLAIISSVAIINVERYYVHVHPMKRYEVRMTLGLVASVYGVWVKALMASVPVYG 180
    |||||||
Db 121 LSVCFVSLAIISSVAIINVERYYVHVHPMKRYEVRMTLGLVASVYGVWVKALMASVPVYG 180
Oy 181 RYSMEGAPSPVPGCSLQMSHSAQCOLFVVPFVAVLYFLPLLLILVVCMSMFRVARVAM 240
    |||||||
Db 181 RYSMEGAPSPVPGCSLQMSHSAQCOLFVVPFVAVLYFLPLLLILVVCMSMFRVARVAM 240
Oy 241 OHGRLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
    |||||||
Db 241 OHGRLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
Oy 301 LPYFSFHLVVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
    |||||||
Db 301 LPYFSFHLVVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
Oy 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSWSVRPLSPKQEPVAVDFRIPQIAE 420
    |||||||
Db 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSWSVRPLSPKQEPVAVDFRIPQIAE 420
Oy 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||
Db 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
```

RESULT 15

```
US-09-714-008A-100
: Sequence 100, Application US/09714008A
: GENERAL INFORMATION:
: APPLICANT: Dang, Huong T.
: APPLICANT: Chen, Rupong
: APPLICANT: Lowitz, Kevin P.
: TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
: TITLE OF INVENTION: Receptors
: FILE REFERENCE: AREN0086
: CURRENT APPLICATION NUMBER: US/09/714,008A
: CURRENT FILING DATE: 2000-11-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 133
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 100
: LENGTH: 869
: TYPE: PRT
: ORGANISM: Homo sapiens and Rat
US-09-714-008A-100
```

```
Query Match 100.0%; Score 2318; DB 21; Length 869;
Best Local Similarity 100.0%; Pred. No. 3,1e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVBEVGLRDVASESVALFFMLLLDLTAVAGN 60
    |||||||
Db 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVBEVGLRDVASESVALFFMLLLDLTAVAGN 60
Oy 61 AAVMAVIAKTPALRKKEVFEVHFLCLVDLLAALTMLPMLSSSALFDHALFGEVACRLYLE 120
    |||||||
Db 61 AAVMAVIAKTPALRKKEVFEVHFLCLVDLLAALTMLPMLSSSALFDHALFGEVACRLYLE 120
Oy 121 LSVCFVSLAIISSVAIINVERYYVHVHPMKRYEVRMTLGLVASVYGVWVKALMASVPVYG 180
    |||||||
Db 121 LSVCFVSLAIISSVAIINVERYYVHVHPMKRYEVRMTLGLVASVYGVWVKALMASVPVYG 180
Oy 181 RYSMEGAPSPVPGCSLQMSHSAQCOLFVVPFVAVLYFLPLLLILVVCMSMFRVARVAM 240
    |||||||
Db 181 RYSMEGAPSPVPGCSLQMSHSAQCOLFVVPFVAVLYFLPLLLILVVCMSMFRVARVAM 240
Oy 241 OHGRLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
    |||||||
```

```
Db 241 OHGRLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
Oy 301 LPYFSFHLVVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
    |||||||
Db 301 LPYFSFHLVVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
Oy 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSWSVRPLSPKQEPVAVDFRIPQIAE 420
    |||||||
Db 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSWSVRPLSPKQEPVAVDFRIPQIAE 420
Oy 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||
Db 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
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Search completed: October 21, 2002, 16:12:45
Job time : 116 secs

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: October 21, 2002, 16:09:30 : Search time 46 Seconds
(without alignments)
2767.495 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318

Sequence: 1 MESSPIPOSSGNSSTIGLRVP.....SDIIMSDSYLRPAAPRLES 451

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1037649 seqs, 282272221 residues

Total number of hits satisfying chosen parameters: 1037649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New :
1: /cgn2_6/ptodata/1/paa/PCIT_NEW.COMB.pep : *
2: /cgn2_6/ptodata/1/paa/US06_NEW.COMB.pep : *
3: /cgn2_6/ptodata/1/paa/US07_NEW.COMB.pep : *
4: /cgn2_6/ptodata/1/paa/US08_NEW.COMB.pep : *
5: /cgn2_6/ptodata/1/paa/US09_NEW.COMB.pep : *
6: /cgn2_6/ptodata/1/paa/US10_NEW.COMB.pep : *
7: /cgn2_6/ptodata/1/paa/US60_NEW.COMB.pep : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2318	100.0	451	1 PCT-US01-03162-2	Sequence 2, Appl1
2	2318	100.0	451	5 US-09-891-138-12	Sequence 12, Appl1
3	2318	100.0	451	5 US-09-891-138A-12	Sequence 12, Appl1
4	2318	100.0	451	6 US-10-088-726-18	Sequence 18, Appl1
5	2318	100.0	451	6 US-10-079-384-2	Sequence 2, Appl1
6	2318	100.0	451	6 US-10-221-160-2	Sequence 2, Appl1
7	2106	90.9	417	6 US-10-219-834-73	Sequence 73, Appl1
8	1276	55.0	252	6 US-10-219-834-74	Sequence 74, Appl1
9	677	29.2	143	6 US-10-221-279-10303	Sequence 10303, A
10	438.5	18.9	368	6 US-10-125-749-10	Sequence 10, Appl1
11	438.5	18.9	368	6 US-10-070-334-1	Sequence 1, Appl1
12	438.5	18.9	368	6 US-10-220-382-4	Sequence 4, Appl1
13	347	15.0	348	7 US-60-389-987-208	Sequence 208, App
14	347	15.0	348	7 US-60-412-418-208	Sequence 208, App
15	337	14.5	400	5 US-09-546-038A-31	Sequence 31, Appl1
16	333	14.4	565	6 US-10-130-461-12	Sequence 12, Appl1
17	332.5	14.3	572	6 US-10-185-991-2	Sequence 2, Appl1
18	332.5	14.3	572	6 US-10-238-129-2	Sequence 2, Appl1
19	332.5	14.3	572	6 US-10-238-667-2	Sequence 2, Appl1
20	325	14.0	501	6 US-10-238-129-7	Sequence 7, Appl1
21	325	14.0	501	6 US-10-238-667-7	Sequence 7, Appl1
22	322.5	13.9	560	6 US-10-238-129-8	Sequence 8, Appl1
23	322.5	13.9	560	6 US-10-238-667-8	Sequence 8, Appl1
24	319.5	13.8	402	7 US-60-389-987-59	Sequence 59, Appl1
25	319.5	13.8	402	7 US-60-412-418-59	Sequence 59, Appl1
26	310	13.4	515	6 US-10-238-129-9	Sequence 9, Appl1

27	310	13.4	515	6 US-10-238-667-9	Sequence 9, Appl1
28	308	13.3	515	6 US-10-130-461-11	Sequence 11, Appl1
29	308	13.3	520	6 US-10-185-991-4	Sequence 4, Appl1
30	308	13.3	520	6 US-10-238-129-4	Sequence 4, Appl1
31	308	13.3	520	6 US-10-238-667-4	Sequence 26, Appl1
32	306	13.2	466	1 PCT-US02-25319-26	Sequence 26, Appl1
33	306	13.2	466	5 US-09-952-680A-26	Sequence 26, Appl1
34	306	13.2	466	6 US-10-002-845-129	Sequence 129, Appl
35	306	13.2	466	6 US-10-215-982-26	Sequence 26, Appl
36	305	13.2	497	5 US-09-568-255-2	Sequence 2, Appl1
37	305	13.2	497	6 US-10-052-589-2	Sequence 2, Appl1
38	305	13.2	515	6 US-10-238-129-10	Sequence 10, Appl
39	305	13.2	515	6 US-10-238-667-10	Sequence 10, Appl
40	300.5	13.0	466	5 US-60-380-336-49	Sequence 49, Appl
41	300	12.9	429	5 US-09-919-039-6	Sequence 6, Appl1
42	300	12.9	466	6 US-10-130-461-10	Sequence 10, Appl
43	300	12.9	466	6 US-10-185-991-6	Sequence 6, Appl1
44	300	12.9	466	6 US-10-238-129-6	Sequence 6, Appl1
45	300	12.9	466	6 US-10-238-667-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
PCT-US01-03162-2
Sequence 2, Application PC/TUS0103162
GENERAL INFORMATION:
APPLICANT: Shyman Ramakrishnan
TITLE OF INVENTION: REGULATION OF HUMAN HISTAMINE H2-LIKE G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 004974.00792
CURRENT APPLICATION NUMBER: PCT/US01/03162
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/190,554
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/210,734
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: 60/255,147
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-03162-2
Query Match 100.0%; Score 2318; DB 1; Length 451;
Best Local Similarity 100.0%; Pred No. 5.3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSPIPOSSGNSSTIGLRVPQTGPSTASGVPEGLRDVASSEVALFFMLLDLTAVAGN 60
|||||
Db 1 MESSPIPOSSGNSSTIGLRVPQTGPSTASGVPEGLRDVASSEVALFFMLLDLTAVAGN 60
QY 61 AAWAVYAKTPALRKFFVPHCLVDLLALTLPLMLSSALFDHALGEGVACRYLFE 120
|||||
Db 61 AAWAVYAKTPALRKFFVPHCLVDLLALTLPLMLSSALFDHALGEGVACRYLFE 120
QY 121 LSVCFVSLATLSVAIVERYYVYVHPMYREVNRTGLVASVYGVVVKALMAASPVIG 180
|||||
Db 121 LSVCFVSLATLSVAIVERYYVYVHPMYREVNRTGLVASVYGVVVKALMAASPVIG 180
QY 181 RVSMEGAPSPPGCSLQMSHAYCOLFVVVFAVLFLPLLLILVYCSMPFVAVVAM 240
|||||
Db 181 RVSMEGAPSPPGCSLQMSHAYCOLFVVVFAVLFLPLLLILVYCSMPFVAVVAM 240
QY 241 QHPPPLTWMTTPRORESLSRSTWYSSGAPOTTTHRTTGGKAAVVLAVGGQFLCW 300
|||||
Db 241 QHPPPLTWMTTPRORESLSRSTWYSSGAPOTTTHRTTGGKAAVVLAVGGQFLCW 300
QY 301 LPYFSHLVVALSAQPISTGQVESVVTWIGYFCFTSNPFYGLNQLNGELSKQVCF 360

|||||
Db 301 LPYFSFHLVYALSAQPISTGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360
Qy 361 KPAPEEELRLPSREGSIEENFLQLOGTGCPSSESVSRPLSPKQEPVADFRI PQGIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQLOGTGCPSSESVSRPLSPKQEPVADFRI PQGIAE 420
Qy 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 2
US-09-891-138-12
Sequence 12, Application US/09891138
GENERAL INFORMATION:
APPLICANT: Lin, Daniel Chi-Hong
APPLICANT: Zhao, Jiaqiang
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Novel Receptors
FILE REFERENCE: 018781-006210US
CURRENT APPLICATION NUMBER: US/09/891,138
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human TGR213 G-protein coupled receptor (GPCR)
US-09-891-138-12

Query Match 100.0%; Score 2318; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 5, 3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
Qy 61 AAVAAVIAKTPALRKFEVFEHLCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Db 61 AAVAAVIAKTPALRKFEVFEHLCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Qy 121 LSVCFVSLATLSVSAINVERYYVHPMRREYRMTGLIVASVGVVWKKALAMASVPLG 180
Db 121 LSVCFVSLATLSVSAINVERYYVHPMRREYRMTGLIVASVGVVWKKALAMASVPLG 180
Qy 181 RVSMEEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLLILVYVCSMFRAVAAM 240
Db 181 RVSMEEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLLILVYVCSMFRAVAAM 240
Qy 241 OHGPLPTMETPRORSSELSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGGQFLCW 300
Db 241 OHGPLPTMETPRORSSELSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGGQFLCW 300
Qy 301 LPYFSFHLVYALSAQPISTGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360
Db 301 LPYFSFHLVYALSAQPISTGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360
Qy 361 KPAPEEELRLPSREGSIEENFLQLOGTGCPSSESVSRPLSPKQEPVADFRI PQGIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQLOGTGCPSSESVSRPLSPKQEPVADFRI PQGIAE 420
Qy 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 3
US-09-891-138A-12
Sequence 12, Application US/09891138A
GENERAL INFORMATION:
APPLICANT: Lin, Daniel Chi-Hong
APPLICANT: Zhao, Jiaqiang
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Novel Receptors
FILE REFERENCE: 018781-006210US
CURRENT APPLICATION NUMBER: US/09/891,138A
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human TGR213 G-protein coupled receptor (GPCR)
US-09-891-138A-12

Query Match 100.0%; Score 2318; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 5, 3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
Qy 61 AAVAAVIAKTPALRKFEVFEHLCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Db 61 AAVAAVIAKTPALRKFEVFEHLCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120
Qy 121 LSVCFVSLATLSVSAINVERYYVHPMRREYRMTGLIVASVGVVWKKALAMASVPLG 180
Db 121 LSVCFVSLATLSVSAINVERYYVHPMRREYRMTGLIVASVGVVWKKALAMASVPLG 180
Qy 181 RVSMEEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLLILVYVCSMFRAVAAM 240
Db 181 RVSMEEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLLILVYVCSMFRAVAAM 240
Qy 241 OHGPLPTMETPRORSSELSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGGQFLCW 300
Db 241 OHGPLPTMETPRORSSELSRSTMTVSSGAPOTTPHRTFGGKAAYVLLAVGGQFLCW 300
Qy 301 LPYFSFHLVYALSAQPISTGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360
Db 301 LPYFSFHLVYALSAQPISTGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360
Qy 361 KPAPEEELRLPSREGSIEENFLQLOGTGCPSSESVSRPLSPKQEPVADFRI PQGIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQLOGTGCPSSESVSRPLSPKQEPVADFRI PQGIAE 420
Qy 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 4
US-10-088-726-18
Sequence 18, Application US/10088726
GENERAL INFORMATION:
APPLICANT: Matsumoto et al.
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 62514
CURRENT APPLICATION NUMBER: US/10/088,726
CURRENT FILING DATE: 2002-03-22

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: PRIOR APPLICATION NUMBER: PCT/JP00/09408
: PRIOR FILING DATE: 2000-12-28      1999-375152
: PRIOR APPLICATION NUMBER: JP
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: JP      2000-101339
: PRIOR FILING DATE: 2000-03-31
: NUMBER OF SEQ ID NOS: 63
: SOFTWARE: Patentn Ver. 2.1
: SEQ ID NO 18
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-088-726-18

Query Match      100.0%: Score 2318: DB 6: Length 451:
Best Local Similarity 100.0%: Pred. No. 5.3e-185:
Matches 451: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MESSPIPOSSGNSSTLGRVPOTPGSTASGVEVGLRDVASSEVALFEMLLDLDLTAIVAGN 60
DB 1 MESSPIPOSSGNSSTLGRVPOTPGSTASGVEVGLRDVASSEVALFEMLLDLDLTAIVAGN 60
QY 61 AAVMAVIKTPALRKRFVFFHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
DB 61 AAVMAVIKTPALRKRFVFFHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
QY 121 LSVCFVSLAIISSVAIINVERYYVHPMKRYEVRMTLGLVASVYGVWVKALAMASVPVLG 180
DB 121 LSVCFVSLAIISSVAIINVERYYVHPMKRYEVRMTLGLVASVYGVWVKALAMASVPVLG 180
QY 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLFLPLLIIIVYCSMRVARVAM 240
DB 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLFLPLLIIIVYCSMRVARVAM 240
QY 241 OHGPLPTMMETPRQSESLSSRSTWVTSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
DB 241 OHGPLPTMMETPRQSESLSSRSTWVTSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
QY 301 LPYFSFHLHYVALSAPISTGQVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
DB 301 LPYFSFHLHYVALSAPISTGQVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 5
US-10-079-384-2
: Sequence 2, Application US/10079384
: GENERAL INFORMATION:
: APPLICANT: Commun1, Didier
: TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
: FILE REFERENCE: 9409/2132
: CURRENT APPLICATION NUMBER: US/10/079,384
: PRIOR FILING DATE: 2002-02-20
: PRIOR APPLICATION NUMBER: US 09/885,453
: PRIOR FILING DATE: 2001-06-20
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Patentn version 3.1
: SEQ ID NO 2
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-079-384-2

Query Match      100.0%: Score 2318: DB 6: Length 451:
Best Local Similarity 100.0%: Pred. No. 5.3e-185:
Matches 451: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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QY 1 MESSPIPOSSGNSSTLGRVPOTPGSTASGVEVGLRDVASSEVALFEMLLDLDLTAIVAGN 60
DB 1 MESSPIPOSSGNSSTLGRVPOTPGSTASGVEVGLRDVASSEVALFEMLLDLDLTAIVAGN 60
QY 61 AAVMAVIKTPALRKRFVFFHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
DB 61 AAVMAVIKTPALRKRFVFFHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
QY 121 LSVCFVSLAIISSVAIINVERYYVHPMKRYEVRMTLGLVASVYGVWVKALAMASVPVLG 180
DB 121 LSVCFVSLAIISSVAIINVERYYVHPMKRYEVRMTLGLVASVYGVWVKALAMASVPVLG 180
QY 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLFLPLLIIIVYCSMRVARVAM 240
DB 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLFLPLLIIIVYCSMRVARVAM 240
QY 241 OHGPLPTMMETPRQSESLSSRSTWVTSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
DB 241 OHGPLPTMMETPRQSESLSSRSTWVTSSGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
QY 301 LPYFSFHLHYVALSAPISTGQVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
DB 301 LPYFSFHLHYVALSAPISTGQVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 6
US-10-221-160-2
: Sequence 2, Application US/10221160
: GENERAL INFORMATION:
: APPLICANT: Shyman Ramakrishnan
: TITLE OF INVENTION: REGULATION OF HUMAN SEROTONIN-LIKE G PROTEIN-COUPLED
: FILE REFERENCE: 004974.00791
: CURRENT APPLICATION NUMBER: US/10/221,160
: PRIOR FILING DATE: 2002-09-18
: PRIOR APPLICATION NUMBER: US 60/190,194
: PRIOR FILING DATE: 2000-03-20
: PRIOR APPLICATION NUMBER: US 60/210,975
: PRIOR FILING DATE: 2000-06-12
: PRIOR APPLICATION NUMBER: US 60/255,110
: PRIOR FILING DATE: 2000-12-14
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: Patentn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-221-160-2

Query Match      100.0%: Score 2318: DB 6: Length 451:
Best Local Similarity 100.0%: Pred. No. 5.3e-185:
Matches 451: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MESSPIPOSSGNSSTLGRVPOTPGSTASGVEVGLRDVASSEVALFEMLLDLDLTAIVAGN 60
DB 1 MESSPIPOSSGNSSTLGRVPOTPGSTASGVEVGLRDVASSEVALFEMLLDLDLTAIVAGN 60
QY 61 AAVMAVIKTPALRKRFVFFHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
DB 61 AAVMAVIKTPALRKRFVFFHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
QY 121 LSVCFVSLAIISSVAIINVERYYVHPMKRYEVRMTLGLVASVYGVWVKALAMASVPVLG 180
DB 121 LSVCFVSLAIISSVAIINVERYYVHPMKRYEVRMTLGLVASVYGVWVKALAMASVPVLG 180
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: CURRENT FILING DATE: 2002-09-06
: PRIOR APPLICATION NUMBER: 09/574,454
: PRIOR FILING DATE: 2000-05-19
: PRIOR APPLICATION NUMBER: 09/519,705
: PRIOR FILING DATE: 2000-03-07
: NUMBER OF SEQ ID NOS: 12360
: SOFTWARE: Custom
: SEQ ID NO 10303
: LENGTH: 143
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-221-279-10303

Query Match          29.2%; Score 677; DB 6; Length 143;
Best Local Similarity 95.5%; Pred. No. 1.2e-48;
Matches 126; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 313 SAQPISTGQVESVWVGIFGFTSNPFYGCINROIIGELSKQFVCFKPADEELRLPS 372
DB 1 SAQPISTGQVESVWVGIFGFTSNPFYGCINROIIGELSKQFVCFKPADEELRLPS 60

QY 373 REGSIEENFLQGTGCPSESWSRPLPSKQEPFPAVDRIIPGOIAETSEFLDQULTS 432
DB 61 REGSIEENFLQGTGCPSESWSRPLPSKQEPFPAVDRIIPGOIAETSEFLDQULTS 120

QY 433 DIIMSDSYLRPA 444
DB 121 DIITNSTYLSLA 132

RESULT 10
US-10-125-749-10
: Sequence 10, Application US/10125749
: GENERAL INFORMATION:
: APPLICANT: Erding Hu
: APPLICANT: Yuan Zhu
: APPLICANT: Ganesh M. Sathe
: APPLICANT: Joyce Yue Mao
: APPLICANT: Wendy S. Halsey
: APPLICANT: Jon Chambers
: APPLICANT: Allison Isobel Muir
: APPLICANT: Philip Graham Szekeres
: APPLICANT: Usman Shabon
: APPLICANT: Derek J. Bergsma
: APPLICANT: Nabil A. Elshourbagy
: APPLICANT: David Michalovich
: APPLICANT: Pamela A. Lane
: APPLICANT: Menelaos N. Pangalos
: APPLICANT: Melanie Robbins
: APPLICANT: David Malcolm Duckworth
: APPLICANT: Jeffrey Hill
: APPLICANT: Ping Tsui
: APPLICANT: Pankaj Agarwal
: APPLICANT: Randall Forrest Smith
: APPLICANT: Lisa Vawter
: APPLICANT: Catherine E. Ellis
: APPLICANT: Manhandeshwar Gattu
: APPLICANT: John W. Quillen, Jr.
: APPLICANT: Erin M. Toland
: APPLICANT: Steven Michael Foord
: APPLICANT: Han Ngoc Trinh
: APPLICANT: Alexander Taylor
: APPLICANT: Henry Sarau
: APPLICANT: Steven Ruben
: APPLICANT: George H. Poste
: APPLICANT: Michel Louis Souchet
: APPLICANT: Philippe Laurent Robert
: APPLICANT: Stephane Clement Krief
: APPLICANT: Bernard Emile Joseph Gout
: APPLICANT: Eve Mane
: TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
: TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
: FILE REFERENCE: GP-70775B-C1
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: CURRENT APPLICATION NUMBER: US/10/125,749
: CURRENT FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US/09/988,922
: PRIOR FILING DATE: 2001-11-19
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 368
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-10-125-749-10

Query Match          18.9%; Score 438.5; DB 6; Length 368;
Best Local Similarity 31.8%; Pred. No. 2.9e-28;
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFPMLLDLTAVAGNAVMVIAKTALRKFFVVFHLCVLDLALTLML 96
DB 9 ASEVAGSIGLLIAAVEGALLNGALLVVRTGRLALYLAHLGVVDLLAASIMPL 68

QY 97 AMLSSAL-FDHALFGEVACRLYLFLSVCFVSLAIIISVAIVERIYVYVHPMKREVRMT 155
DB 69 GLIAAPPGLGRVRLGPAPCRARFSLAALLPACTLGVALGLIARYRLIVHPLRGSSRP 128

QY 156 LGLVASVLGVVVKALAMASVPLGRVSMEGAPSVPPCCSLQWSHSAVCOL-----F 208
DB 129 PVL---VLTAVMAAGLGALSL-----GPPAPPA-----PARCSVLAGLCP 172

QY 209 VVFAVLYFLPLLLILVYVCSMPFRVAVAMOHGPLPTMETPPRORESLSRSTMYTS 268
DB 173 RPLMALFLALPALLLLGAYGSIYVARRAALR-PPRA--RGSRLRSDLSRLSIL-- 227

QY 269 SGAPOTTPHRTGGKAAVYLLAVGGQFLCMLPFPSFHLVYALSQPISTGQVESVWTW 328
DB 228 ---PPLRPR--LPGKAALAPALAVGOFAMCWLPLY---GCACIAPARAABAAVATW 277

QY 329 IGYFCTSNPFYGCINROIIR---GELSKQFVCFKPADEELRLPSREGSIEENFLQFL 385
DB 278 VAYSAPAAHPFLYGLQRPVRLALGRLSRRAL-----PGVVR----- 314

QY 386 OCTGCPSESWSRPLPSKQEPFPAVDRIIPGOIAETSE 424
DB 315 ---ACTPGAMHPRALLQCGRPBPBPVGPSPSAPDPTPE 350

RESULT 11
US-10-070-334-1
: Sequence 1, Application US/10070334
: GENERAL INFORMATION:
: APPLICANT: WATANABE, TAKUYA
: APPLICANT: KIKUCHI, KUNIKO
: APPLICANT: SHINTANI, YASUSHI
: TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA
: FILE REFERENCE: 57126(46342)
: CURRENT APPLICATION NUMBER: US/10/070,334
: CURRENT FILING DATE: 2002-07-12
: PRIOR APPLICATION NUMBER: PCT/JP00/05663
: PRIOR FILING DATE: 2000-08-08
: PRIOR APPLICATION NUMBER: JP 11-241529
: PRIOR FILING DATE: 1999-08-27
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 368
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-070-334-1

Query Match          18.9%; Score 438.5; DB 6; Length 368;
Best Local Similarity 31.8%; Pred. No. 2.9e-28;
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;
```

[illegible]

```

Db      9  ASEVAGSLGILLAAVNEVEGALLGNGALLVVLRRPGRBDALYLAHLCEVDDLLAAASTMPL 68
Qy      97  AMLSSAL-FDHAFGEVYACLYIFLVSCEVSLAILTSYSAINERYVVVYHPMKREYRMT 155
      : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      69  GLTAAAPPGLGRVRRGPRCAARFREFLSAALLPACTTLCVAAIGLGRILYIHPLRGSRPP 128
Qy      156  LGIVASVLYGVWVKALMAASVPYLVGRYSWEGASVPPGCSLQMSHAYCOL-----F 208
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      129  PVL---VLTAWAAGLGLGALSL-----GPPAPPPA-----PARCSVLAGLGPF 172
Qy      209  VVFEAVTFLPLRLIIIVVYCSMFVRVAAVAAOHGPLPTWMETPRQRESLSKSTWTS 268
      : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      173  RPLWALLAFALPALLLLGAYGIFVVARAALR-PPRA--RGRSLRSDSLDSLTL-- 227
Qy      269  SGAPQTPPHRTFEGGKAVALVLLVAGGOFLLCMLPYFSFHLVVALSAOPISTGOVESVYTW 328
      : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      228  --PLPRR-LPGKALALPALAVGEPAAWCLPY-----GCACLTAAARAAEAEAAVYTW 277
Qy      329  IGYFTCTNPFYFGCLNMQIR---GELSKQVCCFKAPREBELLPBREGSIEENFLOFL 365
      : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      278  VAYSAFAHPPLLYGLQRPVLAIGRLSRRL-----GQPRV----- 314
Qy      386  QQTGCPSESQVSRPLPSRKPQBPVDFRIPQIAEETSE 424
      : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      315  ---ACTPQAHHPRALLOCTQLRPPREGVAPGVPSEAEAPQPR 350

```

```

RESULT 12
US-10-220-382-4
; Sequence 4, Application US/10220382
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: VAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dying Alina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/10/220,382
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBERS: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2289894CD1
US-10-220-382-4

```

```

RESULT 13
US-60-389-987-208
; Sequence 208, Application US/60389987
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojn D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465P2
; CURRENT APPLICATION NUMBER: US/60/389,987
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-208

Query Match          15.0%: Score 347; DB 7; Length 348;
Best Local Similarity 28.6%: Pred. No. 1.2e-20;
Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10.

DQ      49  MLLDLTFVAGNAAMAVYAKTPALRKFFV--FVFHICLVLDLAAALPLMLSSALFD 106
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      22  LAVLLITVAGNVVYGLAVGLNRRLRNLTNCITVSLAIITDLLGLVLFP-----SAIQ 76

DQ      107 HAL---FEEVACRLYLFLSVCFVSLAISVSAINVERYYYVVPKREYVRMTLGLVASYL 163
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      77  LSCKMSFGKVCNITVSLDVMCTASILNLFMISLDRCAYAMDPLRYPLVTPARVAISL 136

DQ      164 VGWVKALAMASVPV-LGRVSNBEGAPS--VPPGCSLQWSHSAYCOLFVYVFAVLYFLFP 220
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      137 VLVIVISTLISFLSLHLGWNSENRETSKGNHTSKCNVQVN-----EYVGLVDGLVTFYLP 191

```

Query Match	18.9%	Score 438.5;	DB 6;	Length 368;
Best Local Similarity	31.8%;	Pred. NO. 2.9e-28;		
Matches 127; Conservative	55;	Mismatches 146;	Indels 71;	Gaps 14;
QY	40 ASE---	STALFFMLLDLTAVAGNAAVAVIKTALRKFVVFHLCVLDLALTIMPL	96	

[illegible]

Db 229 ----ATVTLAAMGAFIICMPPEYFAFYRGLRGDDAINEMLEAIVLWGYANSALNPIL 284
Oy 341 YGCLNROIRGELSOFVCFKPAPEBELRPSREG---SIEENFLO 383
Db 285 YALNRPDRTGYOQLFCC-----RLANRSHKTSLSNASQ 320

RESULT 14

US-60-412-418-208
Sequence 208, Application US/60412418
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P3
CURRENT APPLICATION NUMBER: US/60/412.418
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-60-412-418-208

Query Match 15.0% Score 347; DB 7; Length 348;
Best Local Similarity 28.6% Pred. No. 1.2e-20;

Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10;

Oy 49 MLLDLTAAGNAVMAYIAKTPALRKFEV--FVPHLCVLDLAALTMPLMLSSALFD 106
Db 22 LAVILITVAGNVVYCLAVGLNRRLNTNCFIVSLATDILLGLVLPF-----SAIQ 76
Oy 107 HAL---FGEVACRLYLFSVCFVSLAISVSAINVERIYVHPKRYEVRMTGLVASVL 163
Db 77 LSCRMSEFGKVCNITYTSLDVMCLTASINLPMISLDRYCAVMDPLRYEVLTPARVAISL 136
Oy 164 VGWVWKALAMASVPY-LGRVSMEGAPS--VPGCCSLQMSHSAVQQLFVVVFAVLXFLP 220
Db 137 VLIWVISTISFLSHLQMSRNETSKGNHTTSKCNVYN-----EVLGDGLVTFYLP 191
Oy 221 LLLILVYCSMFYARVAAMOHGRLPTWMTTPRORSESLSSRSTWVTSSGAPQTPHRTF 280
Db 192 LLIMCIFYRIFRYARDOAKRIDHSSWK-----AATIREHR-- 228
Oy 281 GGGAAVAVVLLAVGQGLLCMLPIFYSFHLIYVALSAOPISTGOVESVYTWIGYFCFTSNPFF 340
Db 229 ---ATVTLAAMGAFIICMPPEYFAFYRGLRGDDAINEMLEAIVLWGYANSALNPIL 284
Oy 341 YGCLNROIRGELSOFVCFKPAPEBELRPSREG---SIEENFLO 383
Db 285 YALNRPDRTGYOQLFCC-----RLANRSHKTSLSNASQ 320

RESULT 15

US-09-546-038A-31
Sequence 31, Application US/09546038A
GENERAL INFORMATION:
APPLICANT: Gould-Rothberg, Bonnie
TITLE OF INVENTION: METHOD OF IDENTIFYING LIGANDS FOR THE PEROXISOME
TITLE OF INVENTION: PROLIFERATOR ACTIVATED RECEPTOR GAMMA USING
TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION
FILE REFERENCE: 15966-546 METHOD OF IDENTIFYING LIGAND
CURRENT APPLICATION NUMBER: US/09/546.038A
CURRENT FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: USSN 60/130.821
PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 400
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-546-038A-31

Query Match 14.5% Score 337; DB 5; Length 400;
Best Local Similarity 28.2% Pred. No. 9.5e-20;

Matches 120; Conservative 65; Mismatches 168; Indels 52; Gaps 17;

Oy 4 SPIPOSSGNSSTLGRVPQ--TPGSPASGVPEUGLRDVAESVALFEMLLDUTAVAGNAA 62
Db 2 APWPKKNGSLAFWSDAPPLDPSAANTSGLPVY-----PMAALAGALLALATVGGHLL 54
Oy 63 VMAVIKTPALRKFEV--FVPHLCVLDLAALTMPLMLSSALFDHALFGEVACRLYLF 120
Db 55 VITAIARPRLOTTITNVEVTSLATPADLVGLVMPG--ATLALUHGHPGATGCELMTS 112
Oy 121 LSCFVSLAISVSAINVERIYVHPKRYEVRMTGLVASVLYGVWVKALAMASVPVLG 180
Db 113 VDVLCTVTAISIEITLCAVADRYLATVNPRLYGLTVTKRRARAAYVLMIVSATVSPAPIMS 172
Oy 181 RVSMEGAPSVPPGCCSLQMSHSAVQQL-----FVVVFAVLXFLPILLILVYCSMPRYA 235
Db 173 Q-WMRVGADAERQCH---SNPRCCSFASNMPTALLSSVSFYLPLVLMLEFVARFVYA 228
Oy 236 ---RVAAMOHGRLPTWMTTPR--ORSESLSSRSTWVTSSGAPQ--TPHNR--TFGGGKA 285
Db 229 KRORRLRRELGRFP--EESPRSPSPSPATVGTPTASDGVPSGRRPARLPLGEMRA 287
Oy 286 AVVLLAVGQGLLCMLPIFYSFHLIYVALSAOPISTGOVESVYTWIGYFCFTSNPFFYGLN 345
Db 288 LRTGLIMGIFSLCMLPFLFANVLAIVGSLVPSGVYIALNWLGAANSAPNPPLY-CRS 346
Oy 346 ROIRGELSOFVCFKPAPEBELR-----LPSREGSIEENFLOFLOGTGCPSESWS 397
Db 347 PDFR-DARRLICSTYGGNGPEEPKRYVTPASPVSARONSPLNRF-----DGYEGE---- 395
Oy 398 RPLPS 402
Db 396 RPPPT 400

Search completed: October 21, 2002, 16:13:37
Job time : 47 secs

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PF 29-MAR-2001: 2001WO-US10436.
XX
XX 29-MAR-2000: 2000US-193051P.
PR 06-APR-2000: 2000US-195155P.
PR 20-APR-2000: 2000US-199084P.
PR 28-APR-2000: 2000US-200551P.
PR 03-MAY-2000: 2000US-202278P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA,
PI Nguyen DB, Patterson C, Lai P, Au-young J, Yang J, Hafalia A;
PI Walla NK, Das D:
XX
XX WPI: 2001-616472/71.
DR N-PSDB: AAD19579.
XX
XX New human G-protein coupled receptors, useful for treatment and
PT diagnosis of e.g. cell proliferation, also screening for specific
PT modulators, and related nucleic acid
XX
XX
XX Claim 1: Page 104-105; 111pp; English.
XX
XX The present sequence is a human G-protein coupled receptor, GCRC-3
CC protein. The GCRCs are used for treating or preventing disorders
CC associated with decreased expression of functional GCRC, and for
CC identifying specific agonists and antagonists, also binding agents
CC and modulators. They can also be used for generating specific antibodies
CC and for proteosome analysis. Disorders that can be treated include
CC cell proliferative disorders, e.g., arteriosclerosis and cancer,
CC neurological disorders, e.g., Huntington's disease and Parkinson's
CC disease, cardiovascular disorders, e.g., atherosclerosis and congestive
CC heart failure, gastrointestinal disorders, e.g., gastritis and nausea,
CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
CC syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
CC obesity and viral infections. Nucleic acids that encode GCRC are
CC used for identifying agents that alter its expression, for assessing
CC toxicity of test compounds, and as sources of primers and probes for
CC diagnostic detection of GCRC DNA and of therapeutic antisense and
CC ribozyme sequences. They can also be used in gene therapy, for
CC chromosome mapping, and for recombinant production of GCRC. The
CC antibodies are useful for diagnosis and monitoring of diseases
CC associated with GCRC expression, for detecting and purifying GCRC,
CC and as therapeutic agents and for drug screening.
CC
XX
XX Sequence 451 AA:
SQ

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DB 301 LPYFSFHLVVALSADPISTGQVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQFVCF 360
OY 361 KPAPBEELRLPREGSIEENFLQGTGCPSESWSRPLPSPKOPPAVDRIPOQIAE 420
DB 361 KPAPBEELRLPREGSIEENFLQGTGCPSESWSRPLPSPKOPPAVDRIPOQIAE 420
OY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 2
AAU07900
ID AAU07900 standard; Protein: 451 AA.
AC AAU07900;
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human serotonin-like G protein-coupled receptor (5-HT-GPCR).
DE
XX
XX Human; serotonin-like G protein-coupled receptor; 5-HT-GPCR;
KW peripheral nervous system; central nervous system; PNS; CNS;
KW brain injury; mood disorder; anxiety disorder; sleep disorder;
KW neurogenic; myopathic disorder; neurodegenerative disorder;
KW tranquilizer; nootropic; neuroprotective; antiparkinsonian;
KW analgesic; cerebroprotective.
XX
XX Homo sapiens.
OS
XX
XX WO200170967-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 19-MAR-2001; 2001WO-EP03117.
PF
XX
XX 20-MAR-2000; 2000US-190104P.
PR 12-JUN-2000; 2000US-210975P.
PR 14-DEC-2000; 2000US-255110P.
XX
XX (FARB ) BAYER AG.
PA
XX
XX Ramakrishnan S;
PI
XX
XX WPI: 2001-611498/70.
DR N-PSDB: AAS12583.
XX
XX New polynucleotide encoding a polypeptide which regulates, prevents and
PT treats diseases of the peripheral or central nervous system including
PT Alzheimer's Disease, comprises the human serotonin-like G
PT protein-coupled receptor polynucleotide
XX
XX Claim 1: Fig 2; 88pp; English.
XX
XX The present invention relates to the isolation of a novel DNA sequence
CC encoding a human serotonin-like G protein-coupled receptor (5-HT-GPCR)
CC polypeptide. The sequences of the invention are useful for screening for
CC agents which decrease the activity of 5-HT-GPCR or for identifying agents
CC which regulate the activity of 5-HT-GPCR. A reagent that modulates the
CC activity of 5-HT-GPCR is useful for detecting 5-HT-GPCR in a biological
CC sample and for reducing the activity of 5-HT-GPCR in a cell. A
CC pharmaceutical composition comprising such a reagent is useful for
CC preventing or ameliorating disorders of the peripheral or central nervous
CC system, preferably primary or secondary disorders after brain injury,
CC mood disorders, anxiety disorders, disorders of thought and volition,
CC sleep disorders, diseases of the motor unit such as neurogenic and
CC myopathic disorders, neurodegenerative disorders (e.g. Alzheimer's
CC disease, Parkinson's disease) or disorders leading to peripheral and
CC chronic pain. The coding sequence of 5-HT-GPCR polynucleotide is useful
CC for generating antisense oligonucleotides or ribozymes which specifically
CC bind to mRNA transcribed from the 5-HT-GPCR polynucleotide. These
CC antisense oligonucleotides are useful for modulating 5-HT-GPCR gene
CC expression. Polynucleotide sequences encoding for 5-HT-GPCR may be used

```

CC In gene therapy. The present sequence represents the novel human
 CC 5-HT-GPCR polypeptide of the invention.

XX Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 2e-228;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVQTPPGSTAGVPEVGLRDVASSEVALFFMLLDLTAIVAGN 60
 DB 1 MESSPIPOSSGNSSTLGRVQTPPGSTAGVPEVGLRDVASSEVALFFMLLDLTAIVAGN 60
 QY 61 AAVMAVIATPALRKVFVFHCLVDLLAALTPLAMLSSSLPFDHALFGEVACRLTYF 120
 DB 61 AAVMAVIATPALRKVFVFHCLVDLLAALTPLAMLSSSLPFDHALFGEVACRLTYF 120
 QY 121 LSVCFVSLAITSVAINVERYYYVHPMRYEVRMTLGLVASVLYGVWVKALAMASVPVLG 180
 DB 121 LSVCFVSLAITSVAINVERYYYVHPMRYEVRMTLGLVASVLYGVWVKALAMASVPVLG 180
 QY 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMFRVARVAM 240
 DB 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMFRVARVAM 240
 QY 241 OHGPLPTWMEFRORSESLSSRTWTSSGAPQTPHRTFEGGKAIVLLAVGGOFLLGW 300
 DB 241 OHGPLPTWMEFRORSESLSSRTWTSSGAPQTPHRTFEGGKAIVLLAVGGOFLLGW 300
 QY 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360
 DB 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360
 QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCCPSESWSRPLPSKOPPAVDRIPOQIAE 420
 DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCCPSESWSRPLPSKOPPAVDRIPOQIAE 420
 QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
 DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 3

AAU08710 standard; Protein: 451 AA.

AC AAU08710;

DT 18-DEC-2001 (first entry)

XX Human histamine H2-like G protein-coupled receptor polypeptide.

XX Histamine H2-like G protein-coupled receptor; histamine H2-like GPCR;
 KW digestive system; immune system; respiratory system; reproductive system;
 KW urinary system; peripheral nervous system; central nervous system; human;
 KW brain injury; mood disorder; anxiety; thought disorder; sleep disorder;
 KW motor unit disease; neurogenic disorder; myopathic disorder; neuroleptic;
 KW neurodegenerative disorder; psychotic disorder; cerebrovascular disorder;
 KW Alzheimer's disease; Parkinson's disease; muscle spasm; peripheral pain;
 KW chronic pain; tranquilizer; nootropic; neuroprotective; antiparkinsonian;
 KW analgesic; antidepressant; antiallergic; antiinflammatory; gene therapy;
 KW cerebroprotective; vulnerary.

OS Homo sapiens.

PN WO200170812-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-EP03162.

PR 20-MAR-2000; 2000US-190554P.

PR 12-JUN-2000; 2000US-210734P.

PR 14-DEC-2000; 2000US-255147P.

XX (FARB) BAYER AG.

XX Ramakrishnan S;

DR WPI: 2001-611486/70.

DR N-PSDB: AAS14725.

PT New human histamine H2-like G protein-coupled receptor polynucleotide
 PT and polypeptide which can be regulated for preventing, treating
 PT diseases of digestive, immune, respiratory, reproductive or central
 PT nervous system -

PS Claim 1; Fig 2; 93pp; English.

XX The invention relates to a human histamine H2-like G protein-coupled
 CC receptor (GPCR) polypeptides and the nucleic acids encoding them. The
 CC sequences are useful for screening for agents which regulate the activity
 CC of histamine H2-like GPCR by contacting test compounds with the
 CC polypeptide and monitoring the activity. The polypeptides and their
 CC associated DNA sequences are useful for modulating the activity of a
 CC histamine H2-like GPCR in a disease of the digestive, immune,
 CC respiratory, reproductive, urinary, peripheral or central nervous system,
 CC especially a primary or secondary disorder after brain injury, disorder
 CC of mood, an anxiety disorder, a disorder of thought, a disorder of sleep,
 CC a disease of the motor unit, a neurogenic and myopathic disorder, a
 CC neurodegenerative disorder, a psychotic disorder, a cerebrovascular
 CC disorder, Alzheimer's disease, Parkinson's disease, muscle spasms or a
 CC disorder leading to peripheral and chronic pain. This sequence represents
 CC a human histamine H2-like GPCR polypeptide.

XX Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 2e-228;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVQTPPGSTAGVPEVGLRDVASSEVALFFMLLDLTAIVAGN 60
 DB 1 MESSPIPOSSGNSSTLGRVQTPPGSTAGVPEVGLRDVASSEVALFFMLLDLTAIVAGN 60
 QY 61 AAVMAVIATPALRKVFVFHCLVDLLAALTPLAMLSSSLPFDHALFGEVACRLTYF 120
 DB 61 AAVMAVIATPALRKVFVFHCLVDLLAALTPLAMLSSSLPFDHALFGEVACRLTYF 120
 QY 121 LSVCFVSLAITSVAINVERYYYVHPMRYEVRMTLGLVASVLYGVWVKALAMASVPVLG 180
 DB 121 LSVCFVSLAITSVAINVERYYYVHPMRYEVRMTLGLVASVLYGVWVKALAMASVPVLG 180
 QY 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMFRVARVAM 240
 DB 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMFRVARVAM 240
 QY 241 OHGPLPTWMEFRORSESLSSRTWTSSGAPQTPHRTFEGGKAIVLLAVGGOFLLGW 300
 DB 241 OHGPLPTWMEFRORSESLSSRTWTSSGAPQTPHRTFEGGKAIVLLAVGGOFLLGW 300
 QY 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360
 DB 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360
 QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCCPSESWSRPLPSKOPPAVDRIPOQIAE 420
 DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCCPSESWSRPLPSKOPPAVDRIPOQIAE 420
 QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
 DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 4

AAU04367

ID	AA004367	standard; Protein: 451 AA.
AC	AA004367;	
XX		
XX	23-OCT-2001	(first entry)
DT		
XX		
DE	Human G-protein coupled receptor, hRUP13.	
XX		
KW	Human; G-protein coupled receptor; GPCR, hRUP13; agonist;	
KW	Inverse agonist; lung cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200136471-A2.	
XX		
PD	25-MAY-2001.	
XX		
PE	16-NOV-2000; 2000WO-US31509.	
XX		
PR	17-NOV-1999; 99US-0166088.	
PR	17-NOV-1999; 99US-0166099.	
PR	17-NOV-1999; 99US-0166369.	
PR	23-DEC-1999; 99US-0171900.	
PR	23-DEC-1999; 99US-0171901.	
PR	23-DEC-1999; 99US-0171902.	
PR	11-FEB-2000; 2000US-0181749.	
PR	14-MAR-2000; 2000US-0189258.	
PR	14-MAR-2000; 2000US-0189259.	
PR	10-APR-2000; 2000US-0195888.	
PR	10-APR-2000; 2000US-0195889.	
PR	10-APR-2000; 2000US-0196078.	
PR	28-APR-2000; 2000US-0200419.	
PR	12-MAY-2000; 2000US-0203630.	
PR	12-JUN-2000; 2000US-0210741.	
PR	12-JUN-2000; 2000US-0210982.	
PR	21-AUG-2000; 2000US-0226760.	
PR	26-SEP-2000; 2000US-0235418.	
PR	26-SEP-2000; 2000US-0235779.	
PR	20-OCT-2000; 2000US-0242332.	
PR	20-OCT-2000; 2000US-0242343.	
XX		
PA	(AREN-) ARENA PHARM INC.	
PI	Chen R, Dang HT, Lowltz KP;	
XX		
DR	WPI: 2001-355616/37.	
DR	N-PSDB: AAS07940.	
XX		
PT	Endogenous and non-endogenous versions of human G-protein coupled	
PT	receptors for direct identification of candidate compounds as agonists,	
PT	inverse agonists or partial agonists for use as therapeutic agents -	
XX		
PS	Claim 21; Page 98-100; 160pp; English.	
XX		
CC	The sequence represents a human G-protein coupled receptor (GPCR),	
CC	hRUP13. The endogenous and non-endogenous, constitutively activated	
CC	versions of human G-protein coupled receptors (GPCR), are useful for	
CC	direct identification of candidate compounds having applicability as therapeutic	
CC	agents for treating diseases related to GPCR, e.g. lung cancer.	
CC	Non-endogenous version of human GPCRs are also utilized in research	
CC	settings and in vitro and in vivo system, incorporating GPCRs can be	
CC	utilized to elucidate and understand the roles these receptors	
CC	play in the human condition, both normal and diseased.	
XX		
SO	Sequence 451 AA;	
Query Match	100.0%; Score 2318; DB 22; Length 451;	
Best Local Similarity	100.0%; Pred. No. 2e-228;	
Matches 451; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	

Db	1	MESSTIPQSSGNSSTLIGVPEPTPEPSTRASGVPEVGLADVASEVALFPMILLDLDTAVAGN	60
Qy	61	AAVAVAIAKTPALRKEVFEVFLCLVDLIAALTLMPLAMSSALFDHALFGEVACRLYL	120
Db	61	AAVMAVIAKTPALRKEVFEVFLCLVDLIAALTLMPLAMSSALFDHALFGEVACRLYL	120
Qy	121	LSVCSVSLAIIISVSAINERYVYVHPRRYEVBMIGLVASVLGVWVKKLAMASVPLG	180
Db	121	LSVCFVSLAIIISVSAINERYVYVHPRRYEVBMIGLVASVVLGVWVKKLAMASVPLG	180
Qy	181	RVSMEGAPSVPPGCSLQMSHASVACQLEFVVVFAVLYFLPLLILVYCSMFVARVAAM	240
Db	181	RVSMEGAPSVPPGCSLQMSHASVACQLEFVVVFAVLYFLPLLILVYCSMFVARVAAM	240
Qy	241	QHGLPTMMETPRQSRSELSRSRTMTVSSGAPOTTPTHTPGGKAAYVLLAVGQFFLCW	300
Db	241	QHGLPTMMETPRQSRSELSRSRTMTVSSGAPOTTPTHTPGGKAAYVLLAVGQFFLCW	300
Qy	301	LPYEFHLVYVLSAQPISTGCVESVYTWIGYFCFTSNPFYGCILNRQIRGLSKQFVCF	360
Db	301	LPYEFHLVYVLSAQPISTGCVESVYTWIGYFCFTSNPFYGCILNRQIRGLSKQFVCF	360
Qy	361	KPAPEELRLPSRSGSIEENFLQITGTCPSSESWSRPLSPKQEPAPANDFRITPGIAE	420
Db	361	KPAPEELRLPSRSGSIEENFLQITGTCPSSESWSRPLSPKQEPAPANDFRITPGIAE	420
Qy	421	ETSEFLERQULSTDIIMSDSYLRPAASPLAES 451	
Db	421	ETSEFLERQULSTDIIMSDSYLRPAASPLAES 451	
RESULT 5			
AAG64123			
ID	AAG64123	standard; Protein: 451 AA.	
AC	AAG64123;		
XX	25-SEP-2001	(first entry)	
DT			
XX			
DE	Human G protein-coupled receptor GPRV47.		
XX			
KM	Human; guanosine triphosphate binding protein-coupled receptor;		
KM	G protein-coupled receptor; GPRV; GPRV12; GPRV16; GPRV21; GPRV40;		
KM	GPRV47; GPRV51; GPRV71; GPRV72; cancer; Liver cirrhosis;		
KM	Alzheimer's disease; cytosolic; hepatotropic; neurotropic;		
KM	neuroprotective; gene therapy; peptide therapy.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200148186-A1.		
XX			
PD	05-JUL-2001.		
XX			
PF	28-DEC-2000; 2000WO-JP09408.		
XX			
PR	28-DEC-1999; 99JP-0375152.		
PR	31-MAR-2000; 2000JP-0101339.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;		
PI	Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;		
XX			
DR	WPI: 2001-425662/45.		
XX			
DR	N-PSDB; AAH73514.		
XX			
PT	New DNA encoding guanosine triphosphate binding protein coupled		
PT	receptors and their expression products for screening potential		
PT	anticancer and nootropic drugs and in diagnosis of these diseases		
PS	Example 1; Page 126-129; 170pp; Japanese.		
CC	The invention relates to nine human guanosine triphosphate binding		

CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16, GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the CC genes encoding them. These genes and proteins and antibodies against CC the protein are useful in the treatment, prevention, diagnosis and CC investigation of diseases associated with G protein-coupled receptors, CC including cancer, cirrhosis of the liver and Alzheimer's disease. CC The present sequence is a G protein-coupled receptor of the invention.

XX Sequence 451 AA;

Query Match 100.0%; Score 2318; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 2e-228;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
QY 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120
Db 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120
QY 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180
Db 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180
QY 181 RVSMEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRAVARVAM 240
Db 181 RVSMEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRAVARVAM 240
QY 241 QHGPLEPTMETERPROSESLSSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGQFLICW 300
Db 241 QHGPLEPTMETERPROSESLSSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGQFLICW 300
QY 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RGELSKQVCF 360
Db 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RGELSKQVCF 360
QY 361 KPAPEEELRLPSRGSTIENFLQIGTCGSESVNSRPLSPKQEPAPVDFRIPGQIAE 420
Db 361 KPAPEEELRLPSRGSTIENFLQIGTCGSESVNSRPLSPKQEPAPVDFRIPGQIAE 420
QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 6
AAU04386 standard; Protein: 869 AA.

XX ID AAU04386
XX AC AAU04386;
XX DT 23-OCT-2001 (first entry)
XX DE GPCR-Gs fusion protein, hRUP13-Gs.
XX KW G-protein coupled receptor; GPCR; hRUP13-Gs; agonist;
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Rattus sp.
XX PN W0200136471-A2.
XX PD 25-MAY-2001.
XX PF 16-NOV-2000; 2000WO-US31509.
XX PR 17-NOV-1999; 99US-0166088.
XX PR 17-NOV-1999; 99US-0166099.
XX PR 17-NOV-1999; 99US-0166369.
XX PR 23-DEC-1999; 99US-0171900.

PR 23-DEC-1999; 99US-0171901.
PR 23-DEC-1999; 99US-0171902.
PR 11-FEB-2000; 2000US-0181749.
PR 14-MAR-2000; 2000US-0189258.
PR 14-MAR-2000; 2000US-0189259.
PR 10-APR-2000; 2000US-0195898.
PR 10-APR-2000; 2000US-0195899.
PR 10-APR-2000; 2000US-0196078.
PR 28-APR-2000; 2000US-0200419.
PR 12-MAY-2000; 2000US-0203630.
PR 12-JUN-2000; 2000US-0210741.
PR 12-JUN-2000; 2000US-0210982.
PR 21-AUG-2000; 2000US-0226760.
PR 26-SEP-2000; 2000US-0235418.
PR 26-SEP-2000; 2000US-0235779.
PR 20-OCT-2000; 2000US-0242332.
PR 20-OCT-2000; 2000US-0242343.

(AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Lowitz KP;

WI: 2001-355616/37.
N-PSDB: AAS08271.

PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -
Example 5; Page 146-149; 160pp; English.

CC The sequence is a G-protein coupled receptor (GPCR) fusion protein,
CC hRUP13-Gs, being the human hRUP13 fused to the rat Gs protein.
CC The endogenous and non-endogenous, constitutively activated versions
CC of human G-protein coupled receptors (GPCR), are useful for direct
CC identification of candidate compounds as receptor agonists, inverse
CC agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer.
CC Non-endogenous version of human GPCRs are also utilized in research
CC settings and in vitro and in vivo system, incorporating GPCRs can be
CC utilized to elucidate and understand the roles these receptors
CC play in the human condition, both normal and diseased.

SO Sequence 869 AA;

Query Match 100.0%; Score 2318; DB 22; Length 869;
Best Local Similarity 100.0%; Pred. No. 5e-228;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
QY 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120
Db 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120
QY 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180
Db 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180
QY 181 RVSMEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRAVARVAM 240
Db 181 RVSMEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRAVARVAM 240
QY 241 QHGPLEPTMETERPROSESLSSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGQFLICW 300
Db 241 QHGPLEPTMETERPROSESLSSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGQFLICW 300
QY 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RGELSKQVCF 360
Db 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RGELSKQVCF 360


```
XX New human coupling acceptor and its code sequence - Noabstract
PT Claim 1; Page 16-17 (Disclosure): 22pp; Chinese.
XX
PS The present sequence is the protein sequence for a novel human G protein
CC coupled receptor, BiogPCR31.
CC
XX Sequence 279 AA:
SQ
Query Match 63.5%; Score 1472; DB 22; Length 279;
Best Local Similarity 100.0%; Pred. No. 4.3e-142;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 173 MASPVVLGRVSMGKAPVPGCSLQWMSHAYCOLFVVVFAVLFLPLLILIVYCSMF 232
DB 1 MASPVVLGRVSMGKAPVPGCSLQWMSHAYCOLFVVVFAVLFLPLLILIVYCSMF 60
OY 233 RVARVAAMQHGRLPTWMTPRORSESLSSRSTMTVSSGAPQTPPHRTFGGKAAYVLLAV 292
DB 61 RVARVAAMQHGRLPTWMTPRORSESLSSRSTMTVSSGAPQTPPHRTFGGKAAYVLLAV 120
OY 293 GGQFLICWLPYFSFHLVYALSAQPISTGOVSVTWIGYFCFTSNPFYGCINROIRGEL 352
DB 121 GGQFLICWLPYFSFHLVYALSAQPISTGOVSVTWIGYFCFTSNPFYGCINROIRGEL 180
OY 353 SKQFYCFKRPAPBEELRLPSREGSTEENFLQFLQGTGCPSSWVSRPLPSKQEPAYDF 412
DB 181 SKQFYCFKRPAPBEELRLPSREGSTEENFLQFLQGTGCPSSWVSRPLPSKQEPAYDF 240
OY 413 RIPOQIAETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 241 RIPOQIAETSEFLEQQLTSDIIMSDSYLRPAASPRLES 279
RESULT 9
AAW06595
ID AAW06595 standard; Protein: 252 AA.
XX
AC AAW06595;
XX
DT 17-FEB-1997 (first entry)
XX
DE G protein conjugate receptor protein.
XX
KW G protein conjugate receptor protein; rabbit; amplify;
KW stomach pylorus region smooth muscle cell; primer; PCR.
XX
OS Oryctolagus cuniculus.
XX
PN JP08245697-A.
XX
PD 24-SEP-1996.
XX
PF 16-MAR-1995; 95JP-0057187.
XX
PR 16-MAR-1995; 95JP-0057187.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
DR WPI: 1996-482257/48.
XX
DR N-PSDB; AAT49309.
XX
PT New G protein conjugate receptor protein and related DNA - useful
PT for screening for drugs to inhibit G protein-ligand binding
XX
PS Claim 1; Fig 1 and 2; 25pp; Japanese.
XX
CC This sequence represents a G protein conjugate receptor protein. The
CC region encoding this sequence was purified from rabbit stomach pylorus
CC 11. The G protein conjugate receptor protein may be used in the
CC development of new drugs.
```

```
XX Sequence 252 AA:
SQ
Query Match 55.0%; Score 1276; DB 17; Length 252;
Best Local Similarity 98.0%; Pred. No. 4.3e-122;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 85 VDLAALFLMPLAMSSALFDHALFGVACLYFLSCFVSLAILSVSAINVERYYV 144
DB 1 VDLAALFLMPLAMSSALFDHALFGVACLYFLSCFVSLAILSVSAINVERYYV 60
OY 145 VHPMRVEYRMTLGLVASYLVGVWYKALMASVPVILGRVSMGKAPVPGCSLQWMSHAY 204
DB 61 VHPMRVEYRMTLGLVASYLVGVWYKALMASVPVILGRVSMGKAPVPGCSLQWMSHAY 120
OY 205 COLFVVFVAVLYFLPLLILIVYCSMFRVARVAAMQHGRLPTWMTPRORSESLSSRST 264
DB 121 COLFVVFVAVLYFLPLLILIVYCSMFRVARVAAMQHGRLPTWMTPRORSESLSSRST 180
OY 265 WYSSGAPQTPPHRTFGGKAAYVLLAVGGQFLICWLPYFSFHLVYALSAQPISTGOVES 324
DB 181 WYSSGAPQTPPHRTFGGKAAYVLLAVGGQFLICWLPYFSFHLVYALSAQPIAAGOVEN 240
OY 325 VWTWIGYFCFTS 336
DB 241 VWTWIGYFCFTS 252
RESULT 10
AAR91232
ID AAR91232 standard; Protein: 252 AA.
XX
AC AAR91232;
XX
DT 27-AUG-1996 (first entry)
XX
DE Rabbit G-protein coupled receptor protein portion.
XX
KW G-protein coupled receptor protein; G-PCR; agonist; antagonist;
KW cystic fibrosis; incontinence; diabetes; diagnosis; therapy.
XX
OS Oryctolagus cuniculus.
XX
PN W09605302-A1.
XX
PD 22-FEB-1996.
XX
PF 10-AUG-1995; 95WO-JP01599.
XX
PR 11-AUG-1994; 94JP-0189272.
PR 11-AUG-1994; 94JP-0189273.
PR 11-AUG-1994; 94JP-0189274.
PR 30-SEP-1994; 94JP-0236356.
PR 30-SEP-1994; 94JP-0236357.
PR 02-NOV-1994; 94JP-0270017.
PR 28-DEC-1994; 94JP-0326611.
PR 20-JAN-1995; 95JP-0007177.
PR 16-MAR-1995; 95JP-0057186.
PR 19-APR-1995; 95JP-0093989.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Fujii R, Fukusumi S, Hinuma S, Hosoya M, Ohgi K;
PI Ohkaki T;
XX
DR WPI: 1996-139698/14.
DR N-PSDB; AAT13908.
XX
PT G-protein coupled receptor protein DNA and protein - also methods
PT for isolating (ant)agonists for treatment of cystic fibrosis,
PT incontinence and diabetes
XX
PS Example 16; Page 263-64; 360pp; English.
```

XX A portion (AA91232) of a novel rabbit gastropyloric part smooth
CC muscle-derived G-protein coupled receptor protein (G-PCR) was
CC identified as the product of cDNA clone PMN7 (AA13908). The
CC protein can be obtd. by expression of the encoding cDNA clone in
CC transformed host cells. G-PCRs (see also AA91217-25 and AA91228-33)
CC can be used to screen agonists and antagonists that modulate G-PCR
CC activity, to raise antibodies and to develop assay systems.
XX
SQ Sequence 252 AA:
Query Match 55.0%; Score 1276; DB 17; Length 252;
Best Local Similarity 98.0%; Pred. No. 4.3e-122;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 85 VDLALATLPLMLAMSSSALFDHALFGEVACRLYLFLSYCFSLAITSAINVERYYV 144
DB 1 VDLALATLPLMLAMSSSALFDHALFGEVACRLYLFLSYCFSLAITSAINVERYYV 60
OY 145 VHPMREYRMVLGLVAVSVLVGVKALAMASVPLGRVSWEGADSPGCSLQMSHAY 204
DB 61 VHPMREYRMVLGLVAVSVLVGVKALAMASVPLGRVSWEGADSPGCSLQMSHAY 120
OY 205 COLFVYVAVLYFLPLLLILVYCSMRVARVAAHQCPPLTWMETPRQSESLSSNST 264
DB 121 COLFVYVAVLYFLPLLLILVYCSMRVARVAAHQCPPLTWMETPRQSESLSSNST 180
OY 265 MYTSSGAPOTPHRTFEGGKAHVLLAVGGOFLLCMLPYFSFHLVVALSAOPISIGOVES 324
DB 181 MYTSSGAPOTPHRTFEGGKAHVLLAVGGOFLLCMLPYFSFHLVVALSAOPISIGOVEN 240
OY 325 VVTWIGYFCFTS 336
DB 241 VVTWIGYFCFTS 252

RESULT 11
AA005867
ID AA005867 standard; Protein: 138 AA.
XX
AC AA005867;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 19759.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-514838/56.
XX
DR N-PSDB; AA185798.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX

PS Claim 20; SEQ ID NO 19759; 1399pp + Sequence listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 138 AA:
Query Match 29.9%; Score 692; DB 22; Length 138;
Best Local Similarity 97.7%; Pred. No. 1.2e-62;
Matches 127; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 272 POTTTHRTFEGGKAHVLLAVGGOFLLCMLPYFSFHLVVALSAOPISIGOVESVWTWIGY 331
DB 1 POTTTHRTFEGGKAHVLLAVGGOFLLCMLPYFSFHLVVALSAOPISIGOVESVWTWIGY 60
OY 332 PCFTSNPFYGCGLNQITGELSKOFVCFKPAPEBELRLPSREGSIEENFLOFLOGTGCP 391
DB 61 PCFTSNPFYGCGLNQITGELSKOFVCFKPAPEBELRLPSREGSIEENFLOFLOGTGCP 120
OY 392 SESWVSRLP 401
DB 121 YKSWVSRLP 130

RESULT 12
AAB19523
ID AAB19523 standard; Protein: 368 AA.
XX
AC AAB19523;
XX
DT 09-JAN-2001 (first entry)
XX
DE G protein coupled receptor AXOR23.
XX
KW AXOR23; G protein coupled receptor; 7 transmembrane receptor;
KW TM7 receptor; signal transduction; human; therapy;
KW diagnosis; antibacterial; fungicide; protozoacide; viroicide;
KW cytosstatic; analgesic; antidiabetic; anorectic; antilesthetic;
KW antiparkinsonian; hypotensive; hypertensive; osteopathic;
KW antilanginal; cardiant; cerebroprotective; antiulcer; antiallergic;
KW antimigraine; antiemetic; tranquilizer; neuroleptic; nootropic;
KW anticonvulsant; vaccine.
XX
OS Homo sapiens.
XX
PN WO200053622-A1.
XX
PD 14-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US05230.
XX
PR 09-MAR-1999; 99GB-0005317.
XX
PR 15-SEP-1999; 99US-0396610.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Elshourbagy N, Shabon U, Michalovich D;
XX
DR WPI: 2000-594306/56.
XX
DR N-PSDB; AAA88438.
XX

PT Novel AXOR23 polypeptide and polynucleotides which are members of
PT G-protein coupled (7 transmembrane) receptors for treating infections,
PT pain, cancer, diabetes, obesity, Parkinson's disease and Huntington's
PT disease
XX
XX
PS Claim 1(a): Page 28-29; 34pp; English.
XX
CC The present sequence is that of a novel human G protein coupled (7
CC transmembrane) receptor, termed AXOR23, which shows homology to
CC GPRX OR1A. The invention relates to AXOR23 polypeptides and
CC polynucleotides, recombinant materials and methods for their
CC production. Such polypeptides and polynucleotides are useful for
CC treating bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by HIV-1 or HIV-2, pain, cancer,
CC diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease,
CC acute heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcer,
CC allergy, benign prostatic hypertrophy, migraine, vomiting, psychotic
CC and neurological disorders, and dyskinesias such as Huntington's
CC disease or Gilles de la Tourette's syndrome. They are also useful
CC for identifying agonists and antagonists, which are useful for
CC treating conditions associated with AXOR23 imbalance, as diagnostic
CC reagents, for screening of genetic mutations, for chromosome
CC localization studies, for tissue expression studies, for low
CC capacity screening and in high-throughput screening formats, for
CC identifying membrane bound or soluble receptors, to confound
CC screening methods for detecting the effect of added compounds on
CC the production of mRNA and polypeptide in cells, and as vaccines.
XX
SQ Sequence 368 AA:

Query Match 18.9%; Score 438.5; DB 21; Length 368;
Best Local Similarity 31.8%; Pred. No. 4e-36;
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFEMLLDITAVAGNAAMAVIAKTPALRKFEVFNHLCVLDLAALTLMPL 96
DB 9 ASEVAGSLGLIIAAVEVGALLGNGALLVVLRTPTGLRDALYLALHCVDLLAAASIMPL 68
QY 97 AMUSSAL-FDHALREVAACRLYLFLSVCFVSLALISVSNINVERIYVYHPRREYKMT 155
DB 69 GLIAAPPPLGIVRRLGPAPCRARFLSALLPACTIGVAAALGARLYLHPRPSRPP 128
QY 156 LCLVASVLGVVWKALAMASVPLGRVMEGAPSVPCSLQMSHSAVCOL-----F 208
DB 129 PVL---VLRAVNAAGLLGALSIL-----GPPRAPPPA-----PARCSVLAGLGRP 172
QY 209 VVFAVLYLPLLLILLVYCSMFVRAVAAQHGPLPTWMTPRQRSLSLSRSTMTS 268
DB 173 RPLMALALPALPALLLLGAYGIFVVARRAALR-PPRPA--RGSRLRSDLSRLSIL-- 227
QY 269 SGAPOTTPHRTGGGKAAYVLLAVGQFLCMLPRFSFHLVYVALSQPISTGVESVYTW 328
DB 228 ---PPLRPR--LPGKAALAPALAAVQFAACWLPY-----GCCCLAPARAAMAAEAAVYTW 277
QY 329 IGVFCTSNPFYGYCLNRIQIR---GELSKOVCFEKPAPDEELRLPSRGSTIBENLQFL 385
DB 278 VAYSNAFAPFLYGLQRYVALAGLSRRAL---PGVYR----- 314
QY 386 QGTGCPSESWSRPLPSKQPEPAAVDFRIQGIATSEET 424
DB 315 ---ACTPQAMHPRALLQCLQRPPEGPVAVGPSEAPQETPE 350

RESULT 13
AAV71293
ID AAV71293 standard; Protein; 368 AA.
AC AAV71293;
XX
XX 02-NOV-2000 (first entry)
XX
DE Human orphan G protein-coupled receptor hARE-5.

XX
XX Human: orphan G protein-coupled receptor; GPCR; hARE-5; drug screening;
KW transmembrane receptor; signal cascade.
XX
XX
OS Homo sapiens.
XX
XX WO200031258-A2.
XX
XX 02-JUN-2000.
XX
XX 13-OCT-1999; 99WO-US23687.
XX
XX 20-NOV-1998; 98US-0109213.
XX 16-FEB-1999; 99US-0120416.
XX 26-FEB-1999; 99US-0121852.
XX 12-MAR-1999; 99US-0123946.
XX 12-MAR-1999; 99US-0123949.
XX 28-MAY-1999; 99US-0136436.
XX 28-MAY-1999; 99US-0136437.
XX 28-MAY-1999; 99US-0136439.
XX 28-MAY-1999; 99US-0136567.
XX 28-MAY-1999; 99US-0137127.
XX 28-MAY-1999; 99US-0137131.
XX 29-JUN-1999; 99US-0141448.
XX 29-SEP-1999; 99US-0156555.
XX 29-SEP-1999; 99US-0156633.
XX 29-SEP-1999; 99US-0156634.
XX 29-SEP-1999; 99US-0156653.
XX 01-OCT-1999; 99US-0157280.
XX 01-OCT-1999; 99US-0157281.
XX 01-OCT-1999; 99US-0157282.
XX 01-OCT-1999; 99US-0157293.
XX 01-OCT-1999; 99US-0157294.
XX 12-OCT-1999; 99US-0416760.
XX 12-OCT-1999; 99US-0417044.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Liaw CW, Lin I;
XX WPI; 2000-400068/34.
XX DR N-PSDB; AAD01120.
XX
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
XX for use in the identification of G protein-coupled receptor agonists -
XX
XX Claim 10: Page 50-51; 102pp; English.
XX
XX The present amino acid sequence is the hARE-5, an endogenous human
XX orphan G protein-coupled receptor (GPCR). The full length cDNA was cloned
XX by PCR using hARE-5 specific primers and human genomic DNA as template.
XX The orphan GPCR of the invention, like all GPCRs has seven transmembrane
XX alpha helices with an extracellular N-terminus and an intracellular
XX C-terminus. However, no endogenous ligands has yet been identified for
XX the proteins of the invention. The orphan GPCRs may be used in the
XX identification of their endogenous ligands, and to screen potential GPCR
XX agonists and antagonists for use as pharmaceutical agents. The proteins
XX may also be used in the study of GPCR-mediated signalling cascades, and
XX to elucidate their precise role in normal and diseased human conditions.
XX Nucleic acid encoding human orphan GPCRs may be used for tissue
XX localisation expression analysis to provide information about their
XX function in healthy and pathological states.
XX
XX
SQ Sequence 368 AA:

Query Match 18.9%; Score 438.5; DB 21; Length 368;
Best Local Similarity 31.8%; Pred. No. 4e-36;
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFEMLLDITAVAGNAAMAVIAKTPALRKFEVFNHLCVLDLAALTLMPL 96
DB 9 ASEVAGSLGLIIAAVEVGALLGNGALLVVLRTPTGLRDALYLALHCVDLLAAASIMPL 68

KW schizophrenic disorder; neuroskeletal disorder.
XX Homo sapiens.
OS
XX WO20016742-A2.
PM
XX
XX 13-SEP-2001.
PD
XX
XX 01-MAR-2001; 2001WO-US06814.
PF
XX
XX 03-MAR-2000; 2000US-186854P.
PR
XX 10-MAR-2000; 2000US-188384P.
PR
XX 17-MAR-2000; 2000US-190453P.
PR
XX 20-MAR-2000; 2000US-190730P.
XX
PA (INCYTE GENOMICS INC.
XX
XX Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
PI Lu DAM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J;
PI Harland L, Walsh RT, Lo TP, Borowsky ML;
XX
XX WPI: 2001-656776/75.
DR N-PSDB; AAS15900.
XX
XX
XX Novel G-protein coupled receptor polypeptides, for treating and
PT preventing autoimmune/inflammatory disorders, neurological disorders,
PT cell proliferative disorders, cardiovascular disorders and viral
PT infections -
XX
XX
XX Claim 1; Page 116-117; 141pp; English.
XX
XX The invention describes a novel isolated polypeptide, selected from a
CC group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in
CC vaccines and gene therapy. The polypeptide (I) is useful for screening
CC for agonist or antagonist of (I), compounds specifically binding to (I),
CC or compounds that modulate the activity of (I). The polynucleotide
CC encoding (I) is useful for screening a compound for effectiveness in
CC altering expression of a target polynucleotide comprising (II), by
CC exposing a sample comprising the target polynucleotide to a compound,
CC detecting altered expression of the target polynucleotide, and comparing
CC the expression of the target polynucleotide in the presence of varying
CC amounts of compound and in the absence of the compound. (I) and (II) are
CC useful for diagnosis, treatment and prevention of cell proliferative
CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia,
CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
CC Furthermore, the polynucleotide is useful as primers for detecting
CC single nucleotide polymorphisms; as elements in microarray, to monitor or
CC measure protein-protein interactions, drug-target interactions, and gene
CC expression profiles; to generate a transcript image of a tissue or cell
CC type, and to generate hybridisation probes useful in mapping the
CC naturally occurring genomic sequence. This is the G-protein coupled
CC receptor 4 (GCREC-4), one of 21 GCREC proteins described in the method of
CC the invention.
XX
XX
SQ Sequence 368 AA:
Query Match 18.9%; Score 438.5; DB 22; Length 368;
Best Local Similarity 31.8%; Pred. No. 4e-36;
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

Db 129 PVL---VLTAAVMAAGLGLSL-----GPPAPPPA-----PARCSVLAGLGPF 172
QY 209 VVFAVLFLFLDLLLVYCGSMFVARVAMQHGPPTWMETPRORESLSRSTMTS 268
Db 173 RPLMALAFALPALLLGAYGGIFVVARRAALR-PPRA--RGSRLKSDLSRLSL-- 227
QY 269 SGAPQTPHRTGGGKAADVLLAVGGQFLCLPYFSFLVYALSAQPISTGQVESVYTW 328
Db 228 ---PPLRPR--LPGRAALAPALAVGQFAACWLPY-----GCACLPARAADAEAAVYTW 277
QY 329 IGYFCTSNPFYGCINQIR--GELSKQFYCFKPAPEEELRLPSREGSIEENFLQPL 385
Db 278 VAYSAPFAAHFLYGLQRPVRLALGRLSRAL-----PGPVR----- 314
QY 386 QGTGCPSESWSVRPLPSPKQPPAVDFRIPGIAETSE 424
Db 315 ---ACTPQAMHPRALLQCLQRPPEGPAVGPSEAPEOTPE 350

Search completed: October 21, 2002, 16:09:24
Job time : 38 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:10 ; Search time 17 Seconds
(without alignments)
647.997 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318
Sequence: 1 MESSPIPOSGNSSTLGRVP.....SDIIMSDYLRLPASPRLS 451

Scoring table:

BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents-AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUOS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%	Match	Length	DB	ID	Description
No.	Score						
1	1276	55.0	252	3	US-08-513-974B-52		Sequence 52, Appl
2	1276	55.0	252	3	US-08-513-974B-360		Sequence 360, App
3	351	15.1	358	2	US-08-748-485-6		Sequence 6, Appli
4	350	15.1	359	2	US-08-103-170-7		Sequence 7, Appli
5	349	15.1	359	1	US-07-996-772A-10		Sequence 10, Appli
6	349	15.1	359	2	US-08-748-485-3		Sequence 3, Appli
7	347	15.0	348	4	US-08-875-540-13		Sequence 13, Appli
8	347	15.0	348	4	US-09-171-456-17		Sequence 17, Appli
9	346	14.9	359	2	US-08-103-170-6		Sequence 4, Appli
10	346	14.9	359	2	US-08-103-170-6		Sequence 6, Appli
11	343	14.8	359	2	US-08-748-485-5		Sequence 5, Appli
12	340	14.7	359	2	US-08-467-568-13		Sequence 13, Appli
13	340	14.7	359	2	US-08-748-485-4		Sequence 4, Appli
14	340	14.7	359	2	US-08-103-170-2		Sequence 2, Appli
15	340	14.7	359	2	US-09-030-582-13		Sequence 13, Appli
16	340	14.7	359	3	US-08-875-540-15		Sequence 15, Appli
17	340	14.7	359	4	US-09-171-456-19		Sequence 19, Appli
18	337	14.5	400	1	US-07-916-901-6		Sequence 6, Appli
19	336	14.5	400	1	US-07-783-602C-1		Sequence 1, Appli
20	335.5	14.5	405	1	US-08-351-473B-2		Sequence 2, Appli
21	335	14.5	400	1	US-08-351-473B-4		Sequence 4, Appli
22	332.5	14.3	572	1	US-08-334-698-2		Sequence 2, Appli
23	332.5	14.3	572	1	US-08-228-932-2		Sequence 2, Appli
24	332.5	14.3	572	1	US-08-468-939-2		Sequence 2, Appli
25	332.5	14.3	572	1	US-08-722-001-30		Sequence 30, Appli
26	332.5	14.3	572	1	US-08-406-855A-2		Sequence 2, Appli
27	332.5	14.3	572	2	US-08-722-190-2		Sequence 2, Appli

28	332.5	14.3	572	3	US-08-244-354-2	Sequence 2, Appli
29	332.5	14.3	572	3	US-09-206-899-2	Sequence 2, Appli
30	332.5	14.3	572	5	PCT-US95-0403-2	Sequence 2, Appli
31	326.5	14.1	388	1	US-08-087-772A-2	Sequence 2, Appli
32	326.5	14.1	400	4	US-08-351-473B-5	Sequence 4, Appli
33	326.5	14.1	400	4	US-08-450-962-4	Sequence 4, Appli
34	326.5	14.1	400	4	US-08-450-962-6	Sequence 6, Appli
35	321	13.8	559	2	US-08-406-855A-20	Sequence 20, Appli
36	321	13.8	559	3	US-09-206-899-20	Sequence 20, Appli
37	320	13.8	501	1	US-08-722-001-14	Sequence 14, Appli
38	320	13.8	501	2	US-08-467-568-9	Sequence 9, Appli
39	320	13.8	501	2	US-09-030-582-9	Sequence 9, Appli
40	319.5	13.8	402	1	US-08-444-734A-6	Sequence 6, Appli
41	319.5	13.8	402	1	US-08-087-772A-15	Sequence 15, Appli
42	319.5	13.8	408	1	US-07-916-901-2	Sequence 2, Appli
43	319.5	13.8	408	1	US-08-351-473B-3	Sequence 3, Appli
44	319.5	13.8	408	4	US-08-450-962-2	Sequence 2, Appli
45	319.5	13.8	408	4	US-08-450-962-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-513-974B-52
Sequence 52, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513, 974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357

```

: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236356
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189274
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189273
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189272
: FILING DATE: 11-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Resnick, David S.
: REGISTRATION NUMBER: 34,235
: REFERENCE/DOCKET NUMBER: 45753
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 252 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-513-974B-52
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Query Match          55.0%; Score 1276; DB 3; Length 252;
Best Local Similarity 98.0%; Pred. No. 1,3e-92;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 85 VDLAALTPLMPLAMSSALFDHALFGEVACRLYLFLSCFVSALILSVSAINVERYYV 144
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QY 145 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPVLGRVSWEGAPSPVPGCSLQWHSAY 204
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DB 61 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPVLGRVSWEGAPSPVPGCSLQWHSAY 120
   |||||||
QY 205 COLFVYVFAVLFLPLLLILVYCSMFRVARVAMOGPLPTWMTETROSESLSNST 264
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DB 121 COLFVYVFAVLFLPLLLILVYCSMFRVARVAMOGPLPTWMTETROSESLSNST 180
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QY 265 WTSAGAQPTPHRTFEGGKAAYVLLAVGGQFLCMLPFSPFLYVALSAQPISTGVES 324
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DB 181 WTSAGAQPTPHRTFEGGKAAYVLLAVGGQFLCMLPFSPFLYVALSAQPIAGOVEN 240
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QY 325 VVTWIGYFCFTS 336
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DB 241 VVTWIGYFCFTS 252
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```

RESULT 2
US-08-513-974B-360
: Sequence 360, Application US/08513974B
: Patent No. 6114139
: GENERAL INFORMATION:
: APPLICANT: Hinuma, Shuji
: APPLICANT: Hosoya, Masaki
: APPLICANT: Fujii, Ryo
: APPLICANT: Ohtaki, Tetsuya
: APPLICANT: Fukusumi, Shoji
: APPLICANT: Ohgi, Kazuhiko
: TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
: TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
: NUMBER OF SEQUENCES: 380
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
```

```

: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/513,974B
: FILING DATE: 14-SEP-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP95/01599
: FILING DATE: 10-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-093989
: FILING DATE: 19-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-057186
: FILING DATE: 16-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-007177
: FILING DATE: 20-JAN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-326611
: FILING DATE: 28-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-270017
: FILING DATE: 02-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236357
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236356
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189274
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189273
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189272
: FILING DATE: 11-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Resnick, David S.
: REGISTRATION NUMBER: 34,235
: REFERENCE/DOCKET NUMBER: 45753
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 360:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 252 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-513-974B-360
```

```

Query Match          55.0%; Score 1276; DB 3; Length 252;
Best Local Similarity 98.0%; Pred. No. 1,3e-92;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 85 VDLAALTPLMPLAMSSALFDHALFGEVACRLYLFLSCFVSALILSVSAINVERYYV 144
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DB 1 VDLAALTPLMPLAMSSALFDHALFGEVACRLYLFLSCFVSALILSVSAINVERYYV 60
   |||||||
QY 145 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPVLGRVSWEGAPSPVPGCSLQWHSAY 204
   |||||||
DB 61 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPVLGRVSWEGAPSPVPGCSLQWHSAY 120
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QY 205 COLFVYVFAVLFLPLLLILVYCSMFRVARVAMOGPLPTWMTETROSESLSNST 264
   |||||||
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Db 121 COLFVVFVFAVFLPLLLILVYCSMFVRVAVAAOHGPLEPTMETPRORSESLSSRST 180
Qy 265 WVTSSGAPQTPHRTFEGGKAIVLLAVGGOLFCLMWLPFPHLVVLSAQSISTGVYES 324
Db 181 WVTSSGAPQTPHRTFEGGKAIVLLAVGGOLFCLMWLPFPHLVVLSAQSIAAGOVEN 240
Qy 325 VVTWIGVFCFTS 336
Db 241 VVTWIGVFCFTS 252

RESULT 3
US-08-748-485-6
Sequence 6, Application US/08748485
Patent No. 5817480
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice.
APPLICANT: Guegler, Karl J.
APPLICANT: Goli, Surya K.
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,485
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0159 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 236184
US-08-748-485-6

Query Match 15.1%; Score 351; DB 2; Length 358;
Best Local Similarity 27.5%; Pred. No. 4.1e-20;
Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

Qy 43 SVAFEMLLDLTAVAGNAAMAVIAKTPALRKYV--FVPHLCVLDLLAATLPLMLAMS 100
Db 22 SVVLTLLILI--TIAGNVVVCIAVSLNRRSLTNCFTIVSLAATDLDLGLVLPF---- 74

Qy 101 SSALEFDHAL---FGEVACRLVFLFSCVSLAISVSAINVERYYVYVHPARIEYKRLUG 157
Db 75 -SAIQSLFSTWSPGHVFENVTISLDVMLCTASILNLFMISIDRCVCAVTDPLRPVLPV 133
Qy 158 LVASVLGVWVKALAMASVPIVGRVSWEE-----GAPSVPPGCSLQMSHSAVQCLFVVV 211

Db 134 RVALSLVEFIWVISTILSLST--HIGMNSRNGCTRGNGNFFK--CAVQYN-----EVIQLV 184
Qy 212 FAVLYELLPLLIILVYCSMFVRVAVAAOHGPLEPTMETPRORSESLSSSTWVTSSGA 271
Db 185 DELVTFVPLLLIMCVTYRIFRIAREQAKRINHISMMKAA----- 224
Qy 272 PQTTPHRTFEGGKAIVLLAVGGOLFCLMWLPFPHLVVLSAQSISTGVESVYTWIGY 331
Db 225 -----TIREKATVTLAAVWGAFLICWPFYFAFVYRGLGDDAINEAVEGIVLMWLG 277
Qy 332 FCFTSNPFYGCINROINGELSKOVCPEKFP--APEEELRL-----PSREGSIEENF 381
Db 278 ANSALNPIILYALANRDFRTAQQLEPHCKAFASHNSHKTSRLNLSLPRSQSREGWQLEK 337
Qy 382 LQFLQGTGCPSPESVSRPLPSPKQEP 407
Db 338 PLKIQ-----VMSGTELTHQGNP 356

RESULT 4
US-08-103-170-7
Sequence 7, Application US/08103170
Patent No. 5885824
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Recombinant Genomic Clones Encoding
TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods for Production
TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/633,060
FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-017-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Dog
US-08-103-170-7

Query Match 15.1%; Score 350; DB 2; Length 359;
Best Local Similarity 28.7%; Pred. No. 4.9e-20;
Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

[illegible]

```

US-07-996-772A-10
Sequence 10, Application US/07996772A
Patent No. 547286
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Branchek, Theresa A.
APPLICANT: Weinhank, Richard L.
TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN
RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/996,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 42667/JWP/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: HSF2
US-07-996-772A-10
Query Match 15.1%; Score 349; DB 1; Length 359;
Best Local Similarity 28.7%; Pred. No. 5, 8e-20;

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	Matches	100; Conservative	56; Mismatches	140; Indels	52; Gaps	10;
QY	43	SVALFFMLLDLTAVAGAAVAWYAKTRPALRKVF--FVHICLVLDLALATLMPLAMLS	100			
Db	22	SVVLTVLLI!---TAGWVVVCLAGLNRRLRSLTNCIVSLAIDLLDGLLVLPF----	74			
QY	101	SSALEFDHAL----EGEVACRLYLFISVCVSLAIIISVSAINWERYVVVVHPRMYEVRMTLG	157			
Db	75	-SAFQUSCRMSFCGVFNITYTSLDMVLCSTSIINLFMSIDRYCAVTDPLKYPPLITPV	133			
QY	158	LVASVYGVWVKALMAAGVPV-IGRVSMEGAP--SVPGCSIQMSHSAACOLFVVFAY	214			
Db	134	RVAASVLTIVWISTLSLSTSLHGNMNSKNEHSFNNHTIPKCVQVN-----LVYGLVDGL	188			
QY	215	LYFLPLRLLLLVYCCSMFRVARVAAMQGRPLETMETPRORSESLSSRTVNTSSGAPQT	274			
Db	189	VTEYPLRLVMCTIYYRIKRIADAOKRIHHMSKMAA-----	225			
QY	275	TPHRTFGGKRAVYLLANGOFILCMWLYFESHLYVALSAQPISTGQVESVYTWYIGFCF	334			
Db	226	---TIGCHKATVTLAAVGAFFIIMCFYFVYFVYRGKGDGDAINAEFAVVLWLGVANS	281			
QY	335	TSNPFYECYLRQIUGELSKQFVCFKRAPR--BELRLPSREGSILEEN	380			
Db	282	ALNPPLIATLNDRFTAYQQLFC--RPSHNAQETSLSRNSSQIARN	327			

```

US-RESULT 6: 487-485-5
Sequence 3: Application US/08748485
Patent No. 5817480
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Giegler, Karl J.
APPLICANT: Goli, Surya K.
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,485
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0159 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank

```

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i-CLONE: 163952
US-08-748-485-3

Query Match
Best Local Similarity 15.1%; Score 349; DB 2; Length 359;
Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

OY 43 SVALFFMLLDLTAVAGNAVAIVAKTPALRKFF--FVFNLCVLDLALTLPLMLAMS 100
Db 22 SVLVLTLLIIT---TIGANNVVCVLAAGLNRRLRSJLNCFFISVLAITDILLGLVLPF----74

OY 101 SSALFDHAL--FGEVACRLLELSYCFVSLATLSAISAINVEYXYVYVNHMRREYKRTLG 157
Db 75 -SAFYOLSRMSSEGKFCFCNITYSLDWMCTASLTINLFMISLDRCYCAVTDPLRYPVLTTPV 133

OY 158 LVASVLYGVWVKALMAASVP--LGRVSWEBGAP--SVPGCSLQMSHSAVCOLEFVVFAV 214
Db 134 RVAVSVLIVMVISITLSFLSIHNGMSRNETSFNNTIRKQYVN-----LVGLVDGL 188

OY 215 LYFLPLPLILIVVYCSMFVARYAAMQGBDLPYMTETPRORSESLSSRTMTWTSAGAPOT 274
Db 189 VTFEYPLRLWCITTYVYRIFKIRADQAKRIHHMGSKAA-----225

OY 275 TPNRFFGGKAVVLLAVGQFLCWLPRSFHLYALSAQPISTGOVESYTWIGYFCF 334
Db 226 ---TIGERKAVTVLLAANGAFILICWFYFVYVNGLGDDAINEAFVAVLMLIGYANS 281

OY 335 TSNPFYGGCLNRQIRGELSKQFVCFKPAPE--EELRLPSREGSIREN 380
Db 282 ALNPILYATLNRDPFTAYQQLFRC--RPASHNAQETSLKSNSSQLARN 327

RESULT 7
US-08-875-540-13
Sequence 13, Application US/08875540A
Patent No. 6015888
GENERAL INFORMATION:
APPLICANT: Heath, Paul Roy
APPLICANT: Orange, Paul Richard
APPLICANT: Pearson, Ronald Carl Alan
APPLICANT: Wright, Simon Ralph
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
TITLE OF INVENTION: HUMAN HISTAMINE H2 RECEPTORS
FILE REFERENCE: 09347/002001
CURRENT APPLICATION NUMBER: US/08/875,540A
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/EP96/00397
EARLIER FILING DATE: 1997-01-30
EARLIER APPLICATION NUMBER: GB9503866.7
EARLIER FILING DATE: 1995-01-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-08-875-540-13

Query Match
Best Local Similarity 15.0%; Score 347; DB 3; Length 348;
Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10;

OY 49 MLLDLTAVAGNAVAIVAKTPALRKFF--FVFNLCVLDLALTLPLMLAMSSALPD 106
Db 22 LAVLITVAGNVVVCVLAAGLNRRLNLTNCFIVSLATIDLLGLVLPF-----SAIYQ 76

OY 107 HAL---REEVACRLYLFISYCVSLAALLSVSAINVEYXYVYVNHMRREYKRTLG 163
Db 77 LSCKMSFKVCNITSLDVMCTASLTINLFMISLDRCYCAVMDPLRYPVLTVPARVAISL 136

OY 164 VGWVVKALMAASVP--LGRVSWEBGAP--VPGCSLQMSHSAVCOLEFVVFAVLYFLP 220
Db 137 VLIWVISITLSFLSIHNGMSRNETSCKGNHTTSCKNVQVN-----EYGLVDGLVTFYLP 191

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OY 221 LLLILVYVCSMEFVARVAAHQGRLPTWMTPTQRBSESLSRSTMTSSGAPOTTHRRF 280
Db 192 LLMCTITVRIEFVAVDQAKRIDHISMK-----AATIREHR-- 228
OY 281 GGGKAAVVLAVGGOFLLCMLPFSEFHLVYALSAQPISTGOVESVTWIGYFCFTSNPFE 340
Db 229 ----ATVTLAAVWGAILICMFPEYTFNAVYRGLRGDAIENMLEAIVLMGYANSALNPIL 284
OY 341 YGCLNRQIRGELSQQVCFEKKPAPEELRLPSREG--SIENFIQ 383
Db 285 YAAINRDFRTGYOQLFCC-----RLANRNSHKTSLSRNSAQ 320

RESULT 8
US-09-171-456-17
; Sequence 17, Application US/09171456A
; Patent No. 6346380
; GENERAL INFORMATION:
; APPLICANT: Wright, Simon Ralph
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; TITLE OF INVENTION: DETECTION OF VARIATIONS IN HUMAN H2 RECEPTORS
; FILE REFERENCE: 09347/004001
; CURRENT APPLICATION NUMBER: US/09/171,456A
; EARLIER FILING DATE: 1999-08-03
; EARLIER APPLICATION NUMBER: PCT/GB97/01075
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-171-456-17

Query Match 15.0%; Score 347; DB 4; Length 348;
Best Local Similarity 28.6%; Pred. No. 8,1e-20;
Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10;

OY 49 MLLDLTAVAGNAAMVAVIAKTPALRKFY--FVHLCLVDLLAALTMLPMLSSALFD 106
Db 22 LAVLLITVAVAGVWVVCIAVGLNRLRNLTNCFIVSLAINDLLGLLVLPF-----SAIVQ 76
OY 107 HAL---FGEVACRLFLFLSYCFVSLAISVSAINVERIYVVHPARYEKRMFLGLVASYL 163
Db 77 LSCKMSFGKVFENITYTSLDVMCTASILNLFMISLDRCAVMDPLRYPLVTPARVAISL 136
OY 164 VGVWAKALAMASVP--LGRVSWEGAPS--VPGCSLQMSHSAYQOLFVAVVLYFLRP 220
Db 137 VLIWVISTLSLSTLHGLGNSRNETSKGNHTTSKCAVOVN-----EVLGVDGLVTFYLP 191
OY 221 LLLILVYVCSMEFVARVAAHQGRLPTWMTPTQRBSESLSRSTMTSSGAPOTTHRRF 280
Db 192 LLMCTITVRIEFVAVDQAKRIDHISMK-----AATIREHR-- 228
OY 281 GGGKAAVVLAVGGOFLLCMLPFSEFHLVYALSAQPISTGOVESVTWIGYFCFTSNPFE 340
Db 229 ----ATVTLAAVWGAILICMFPEYTFNAVYRGLRGDAIENMLEAIVLMGYANSALNPIL 284
OY 341 YGCLNRQIRGELSQQVCFEKKPAPEELRLPSREG--SIENFIQ 383
Db 285 YAAINRDFRTGYOQLFCC-----RLANRNSHKTSLSRNSAQ 320

RESULT 9
US-08-103-170-4
; Sequence 4, Application US/08103170
; Patent No. 5885824
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira

```



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US-08-748-485-5
; Sequence 5, Application US/08748485
; Patent No. 5817480
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Goll, Surya K.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,485
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0159 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 791239
; US-08-748-485-5

Query Match          14.8%; Score 343; DB 2; Length 359;
Best Local Similarity 27.0%; Pred. No. 1.7e-19;
Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKFEV--FVFHLCVLDLLAALTPLMLSSALFD 106
DB 25 LILILITVAGVVVCLAVGLNRRLRLNCFIVSLAVTDLLGLVLP-----SAIQ 79
OY 107 HAL---FGEVACRLTYLFSVCFVSLAISVSAINVERIYVVVHPMREYKMTGLVASVL 163
DB 80 LSCKSFSGVFCNITYTSLDVMICTASILNLFMISIDRYCAVMDPLRYPLVTPVVAISL 139
OY 164 VGWVKALAMASVPVIGRVSMEGAPSPG-----CSLQMSHSAVCOLEFVVFAVLYFL 218
DB 140 VLIWVISTLSFLST--HGMNSRNETSKGNDNTIYKCKQVNV-----EYGLVDGLVTFY 192
OY 219 LPLLILIVVYCSMFVARVAAMQHGRLPTWMTETPRQRESESLSSRSTWVTSSGAPQTPPHR 278
DB 193 LPLLIMCTYFRIFRIAREQARRINHISWKAA----- 225
OY 279 TFGGKAHVLLAAGGOLLCLWLPYFSEHLYVALSAQPISTGQVESVYTWIGYFCFTSNP 338
DB 226 TIREKATVTLAAMGAFILCMFPYFYFAVYRGGLGDADAVNEVFDDVLMGLYANSALNP 285
OY 339 FFYGCGLNRQIRGELSKQVCFPKPAPEBELRLP---SREGSIEENFLQGLQTCGPPSSW 395

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DB 286 ILYAALNRDFRFRAYHQLFCC-----RLASHNSHETSLRLNNSQ-LNNSQCEPRW 334
OY 396 -VSRPL 400
DB 335 QEDKPL 340

RESULT 12
US-08-467-568-13
; Sequence 13, Application US/08467568
; Patent No. 5817477
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,568
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-568-13

Query Match          14.7%; Score 340; DB 2; Length 359;
Best Local Similarity 28.0%; Pred. No. 3e-19;
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKFEV--FVFHLCVLDLLAALTPLMLSSALFD 106
DB 25 LAVLITVAGVVVCLAVGLNRRLRLNCFIVSLATIDLLGLVLP-----SAIQ 79
OY 107 HAL---FGEVACRLTYLFSVCFVSLAISVSAINVERIYVVVHPMREYKMTGLVASVL 163
DB 80 LSCKSFSGVFCNITYTSLDVMICTASILNLFMISIDRYCAVMDPLRYPLVTPVVAISL 139
OY 164 VGWVKALAMASVPV-LGRVSMGAPSP--VPPGSLQMSHSAVCOLEFVVFAVLYFLP 220
DB 140 VLIWVISTLSFLST--HGMNSRNETSKGNDNTIYKCKQVNV-----EYGLVDGLVTFY 194
OY 221 LLLILIVVYCSMFVARVAAMQHGRLPTWMTETPRQRESESLSSRSTWVTSSGAPQTPPHR 280
DB 195 LLLIMCTYFRIFKVARDDAKRINHISWKAA-----TI 227
OY 281 GGGKAHVLLAAGGOLLCLWLPYFSEHLYVALSAQPISTGQVESVYTWIGYFCFTSNPFF 340
DB 228 REHKATVTLAAMGAFILCMFPYFYFAVYRGGLGDADAVNEVLEAIVLMGLYANSALNPIL 287

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OY 341 YGCLNRQIRGELSKQVCFKPAPEEELRLPSREG---SIEENFLQ 383
Db 288 YAAINRDERFTGYQOLFCC-----RLANRSHKTSLRNSAQ 323

RESULT 13

US-08-748-485-4
Sequence 4, Application US/08748485
Patent No. 5817480
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Goli, Surya K.
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,485
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0159 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 184088
US-08-748-485-4

Query Match 14.7%, Score 340; DB 2; Length 359;
Best Local Similarity 28.0%, Pred. No. 3e-19;
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTVAGNAAMAVIAKTPALRKFF--FVPHLCVLDLALTLPLMLSSALFD 106
Db 25 LAVLLIVAGNVVCLAVGLNRRLRLNLTNCFIVSLAITDGLGLVLPF-----SAITYQ 79
OY 107 HAL---FGEVACRLYLFVSCFVSALISVSAINERYVYVHPMRYEVRMTGLVASVL 163
Db 80 LSCKSKFGKVCNITSLDVMICTASINLFPMSIDRYCAVMDPLRYVLTVPRAVAISL 139
OY 164 VGWVKALAMASVPV-LGRVSWEGAPS--VPPGCSLQMSHSAVCQLFVVVFAVLVFLP 220
Db 140 VLIWISTITLSLHGLMNSRNETSKGNHTTSKCKVOVN-----EYGLVDGLVTFYLP 194
OY 221 LLLIIVVCSMPRVARVAAHQGLPLTWMETPRORSESSLSNSTVTVSSGAQQTTPHRTF 280
Db 195 LLIMCTIYRIKFAVADQAKRINHISWMAA-----TIT 227

OY 281 GGKRAAVLLAVGGOFLLCMVPEFSFHLVVALSAQPISTGVESVWIGYCFCTSNPF 340
Db 228 REHKATVTLAAVMGAFILCMFPTFAFYRGLRGDDAINLEVAIVMLGTANALNPIIL 287

OY 341 YGCLNRQIRGELSKQVCFKPAPEEELRLPSREG---SIEENFLQ 383
Db 288 YAAINRDERFTGYQOLFCC-----RLANRSHKTSLRNSAQ 323

RESULT 14

US-08-103-170-2
Sequence 2, Application US/08103170
Patent No. 5885824
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Recombinant Genomic Clones Encoding
TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods For Production
TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/633,060
FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavallee, Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-017-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-103-170-2

Query Match 14.7%, Score 340; DB 2; Length 359;
Best Local Similarity 28.0%, Pred. No. 3e-19;
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTVAGNAAMAVIAKTPALRKFF--FVPHLCVLDLALTLPLMLSSALFD 106
Db 25 LAVLLIVAGNVVCLAVGLNRRLRLNLTNCFIVSLAITDGLGLVLPF-----SAITYQ 79
OY 107 HAL---FGEVACRLYLFVSCFVSALISVSAINERYVYVHPMRYEVRMTGLVASVL 163
Db 80 LSCKSKFGKVCNITSLDVMICTASINLFPMSIDRYCAVMDPLRYVLTVPRAVAISL 139
OY 164 VGWVKALAMASVPV-LGRVSWEGAPS--VPPGCSLQMSHSAVCQLFVVVFAVLVFLP 220
Db 140 VLIWISTITLSLHGLMNSRNETSKGNHTTSKCKVOVN-----EYGLVDGLVTFYLP 194

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0Y 221 LLLILVYVCSMEFRVAAVAAMHGSLPTMMEPPEPRQRSSLSLSRIMVYSSAPQPTTHRTF 260
    |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 195 LLLIMCTYTRILFKARQADAKRINHIISSMKAA-----TI 227

0Y 281 GGGKAAVLLVAVGQFLICMLPYRSPFLHYALSAQPISTGQBSVYTWIGYFCPTSNPF 340
    |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 228 REHKATVYTLAAVCAFTICMPYPTAFYRGLRGDDAINEVLEKIVLWLTGYANSALNPIL 287

0Y 341 YGCLNRQIRGELSKQVCFKPAPEEELRLPSREG---SIEENFLQ 383
    |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 288 YALANRDEFTGYQQLFFC-----RLANRSHSTSLRSNASQ 323

```

RESULT 15
US-09-030-582-13
; Sequence 13, Application US/09030582
; Patent No. 5904506

```

1  APPLICANT: SOPPET, DANIEL R
2  TITLE OF INVENTION: ADRENERGIC RECEPTOR
3  NUMBER OF SEQUENCES: 13
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
6  ADDRESSEE: Stewart & Olstein
7  STREET: 6 Becker Farm Road
8  CITY: Roseland
9  STATE: NJ
10 COUNTRY: USA
11 ZIP: 07068-1739
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.30
18
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/030,582
21 FILING DATE:
22 CLASSIFICATION:
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/467,568
26 FILING DATE:
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Ferraro, Gregory D
30 REGISTRATION NUMBER: 36,134
31 REFERENCE/DOCKET NUMBER: 325800-324
32
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 201-994-1740
35 TELEFAX: 201-994-1744
36
37 INFORMATION FOR SEQ ID NO: 13:
38
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 359 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44
45 MOLECULE TYPE: protein
46
47 US-09-030-582-13

```

Query Match	14.7%	Score 340	DB 2	Length 359
Best Local Similarity	28.0%	Pred. No. 3e-19		
Matches 97	Conservative	57	Mismatches 134	Indels 58
			Gaps	9

[illegible]

```
OY      221 LLLILVYCSMFRRARAAAMHGGLPTWMEFPRRRSLSRSRTMTSSCAPQTTTPKTF 280
          |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      195 LLIMCIITYRIFRKVARQDAKRINNISSKWA-----TI 227

OY      281 GGGRAAVVLLAVGOELLICMLPYSPFHLYAALSQAIPSTGVESVYTWIGTCTSNPF 340
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      228 REHKATVTLAVAKGAFIICMPPEFYTAFFYRGRLRGDDAINEVLEIVLMIAGYANSALNPIL 287

OY      341 YGCNLQRIGELSKPWCFCFPAKEDELRJPSREG---STEENPLQ 383
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      268 YAALLRDERTGTQQULEFC-----RIANNRSHTKSISNSNQ 323
```

Search completed: October 21, 2002, 16:09:46
Job time : 19 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:10 : Search time 21 Seconds
(without alignments)
2063.633 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318

Sequence: 1 MESSPIPOSSGNSSTLGRVP.....SDIMSDYLRLPASPRLS 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR-71:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	823	35.5	428	2	151087	G protein-coupled
2	351	15.1	358	2	JQ1278	histamine H2 recep
3	349.5	15.1	440	2	JC5520	serotonin receptor
4	349	15.1	359	2	A39008	histamine H2 recep
5	343	14.8	359	2	JC4120	histamine H2 recep
6	340	14.7	359	2	JH0449	histamine H2 recep
7	338.5	14.6	436	2	JN0591	serotonin receptor
8	337	14.5	400	2	A53281	beta-3-adrenergic
9	336	14.5	400	2	A41679	beta-3-adrenergic
10	335.5	14.5	405	2	S65459	beta-3-adrenergic
11	335	14.5	428	2	A55044	beta-4C-adrenergic
12	332.5	14.3	572	2	I39369	alpha-1A-adrenergic
13	329.5	14.2	437	2	I57942	5-hydroxytryptamini
14	326.5	14.1	400	2	S32804	beta-3-adrenergic
15	324	14.0	414	1	QRH083	beta-3-adrenergic
16	322.5	13.9	418	2	G02953	beta-3-adrenergic
17	322.5	13.9	560	2	A38731	beta-3-adrenergic
18	320	13.8	501	2	JH0447	alpha-1A adrenergic
19	319.5	13.8	408	1	QRH086	alpha-1A-adrenergic
20	317.5	13.7	379	2	JC6178	beta-3-adrenergic
21	308	13.3	517	2	A45121	serotonin receptor
22	305	13.2	515	2	A40491	alpha-1B adrenergic
23	300	12.9	429	2	S65656	alpha-1B-adrenergic
24	300	12.9	466	2	JN0765	alpha-1C-adrenergic
25	300	12.9	499	2	S65657	alpha-1C-adrenergic
26	292.5	12.6	564	2	A38271	alpha-1C-adrenergic
27	292	12.6	466	2	I57959	serotonin receptor
28	291.5	12.6	515	2	JC1525	alpha-1C adrenergic
29	291	12.6	477	2	S71323	alpha-1B-adrenergic

30	290.5	12.5	501	2	T18863	hypothetical prote
31	290	12.5	466	2	A35375	alpha-1-adrenergic
32	289.5	12.5	388	2	JN0605	somatosatin recep
33	285	12.3	446	1	DYH0D1	dopamine receptor
34	284.5	12.3	385	2	S68780	dopamine D1-like r
35	283	12.2	446	2	I47217	dopamine receptor
36	281.5	12.1	384	2	A47249	brain-specific som
37	278	12.0	459	2	A56849	dopamine receptor-
38	277.5	12.0	422	2	I38209	serotonin receptor
39	277.5	12.0	483	2	A25896	beta-adrenergic re
40	277.5	12.0	511	2	S44275	dopamine receptor
41	274	11.8	387	2	I49246	D4 dopamine recept
42	272	11.7	444	2	C55886	dopamine receptor
43	271.5	11.7	448	2	A47519	serotonin receptor
44	270.5	11.6	384	2	JC4629	somatosatin recep
45	270	11.6	402	2	I56595	neurokinin 2 recep

ALIGNMENTS

RESULT 1

151087

G protein-coupled seven-transmembrane receptor - Japanese medaka

C:Species: Oryzias latipes (Japanese medaka)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: 151087

R:Yasuoaka, A.; Abe, K.; Saigo, K.; Arai, S.; Emori, Y.

Biochim. Biophys. Acta 1235, 467-469, 1995

A:Title: Molecular cloning of a fish gene encoding a novel seven-transmembrane recept

A:Reference number: 151087; MWID:95275927

A:Accession: 151087

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-428 <YAS>

A:Cross-references: GB:D43633; NID:g992581; PIDN:BAA07741.1; PID:g992582

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match	35.5%	Score 823;	DB 2;	Length 428;
Best local similarity	42.3%	Pred. No. 3.6e-59;		
Matches 184;	Conservative 81;	Mismatches 142;	Indels 28;	Gaps 11;
QY	2	ESSPI---POSSGNSST--LGRVPTGPTASGVPEVLG----	RDVASSEVALFFMLLL	52
DB	5	KTSPMTSDHSISNFTSGFGPPTVP-----PDGVVTSQSQMKDLFGLCWTL		56
QY	53	DLTVAGNAAMAVIARTPALRKFFVFHCLVDLLAALTMLPLMSSALFPHALFGE		112
DB	57	NLIALMLNTGVMALIAAPHLKRAFYCHLCADVLCAILMLPLGITSSSPFGTVFTI		116
QY	113	VACRLVFLSCVFSVALISVSAINVERYYYVHPMYEVMTLGLVASVVGVMKALA		172
DB	117	LECOVYIFLNVFLWLSITLTALTSVERFYIVHPMYEVMTLINIGVALLIMFKSL		176
QY	173	MASVPVGRVSWERGASVPPGCSLQWSHSAQCQLFFVVAVALYFLPLLLILVYCSMF		232
DB	177	LALVTLEGPMPYGHQSSIAASHCSLHSHSRLRGVFAVLCCVCEFLAPVAVIESVYAVY		236
QY	233	RVAVAAHQGP-LPTWMT--PRORSESSSRSTWYSSGAPD--TPHRTFGGKAAYV		288
DB	237	KVASAALQGVPAVPTMAADSPAKDRSDINSQTTITTTTLTPORLSPEAFSGKAAIT		296
QY	289	LAVGQFLLCWLDPYFSFHLHYVALSAQPISTGVESVVMIGYFCFTSNPFYGCILKROI		348
DB	297	LAFVIGQFLVCWLPDFIFHLQMSLTGSMKSPGDLAEAVNMNLVASSFAVNSFFGLLRQI		356
QY	349	RGLSTK-QVFCFRPADEELRLPDRSGSTIEENLTQLOGTGCSSEWVGRPLSPK-OE		406
DB	357	RDELVFRRCCTVQPV---EIGDSSLGSGFOENLQIORTSSSETHPSFANSNPRNME		413
QY	407	PPAVDFRIQCIAGE 421		

Db 414 NQA--HKIPQIPPE 426

RESULT 2

J01278

histamine H2 receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: J01278

R:Rat, M.; Traiffort, E.; Arrang, J.M.; Leurs, R.; Schwartz, J.C.

Biochem. Biophys. Res. Commun. 179: 1470-1478, 1991

A:Title: Cloning and tissue expression of a rat histamine H2-receptor gene.

A:Reference number: J01278; MUID:92028890

A:Accession: J01278

A:Molecule type: DNA

A:Residues: 1-358 <RNA>

A:Cross-references: GB:S57565; NID:g236183; PIDN:AA819935.1; PID:g236184

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:22-45/Domain: transmembrane #status predicted <TM1>

F:58-81/Domain: transmembrane #status predicted <TM2>

F:93-113/Domain: transmembrane #status predicted <TM3>

F:116-159/Domain: transmembrane #status predicted <TM4>

F:178-203/Domain: transmembrane #status predicted <TM5>

F:234-260/Domain: transmembrane #status predicted <TM6>

F:267-288/Domain: transmembrane #status predicted <TM7>

F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:220,311,315/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 15.1%; Score 351; DB 2; Length 358;

Best Local Similarity 27.5%; Pred. No. 6.3e-21;

Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

43 SVAFPMLLDLTAVAGAAVAIVAKTPALRKFFV--FVPHLCVLDLALTLPLMLLS 100

Db 22 SVLTTLTLR---TIGAVVVYCLAVSLNRRSLNCFIVSLATDLGLGLVLPF---- 74

101 SSALFDHAL---FGEVACRLVFLVCFVSLAISVSAINERYVVVHPKRYEVRMTIG 157

Db 75 -SAIQQLSTWFSFGHVCNITVSLDVMCTASILNFMISLDRCVAVDPLRYPLVLPV 133

158 LVASLVGVVWKALAMASVPLVGRVSMEE-----GAPSVPGCSLQMSHAYCOLFVV 211

Db 134 RVALSLVFIVVITSLTSLST--HLGWSNRGTGNGDTFK--CKVOYN-----EYGLV 184

212 FAVLVFLPLLLILLVVCSMFRAVAAMOHGRLPTWMETPROSSESLSRSTWTSAGA 271

Db 185 DGLVTFPLPLIMCVYTRIKRIARQAKKRNHISMKAA----- 224

272 PQTTPHRTFGGKAAYVLLAVGGFLCWLPRFSFHLVALSAQPISTGQVESVWTWIG 331

Db 225 -----TIREHKATVTLAAVGAFFICMPFYFAFVYRGLRDAINEAVEGIVLMIG 277

332 FCFSPNPFYGCILNRQIRGELSKQVCFERK--APDEELR-----PSREGSIENF 381

Db 278 ANSALNPLLYALNRDFTAVQQLFHCKFASHSHKTSRLNLSLPRSGREGRMDEK 337

382 LQFLQGTGCPSESWSRPLPSKQEP 407

Db 338 PLKLD-----VMSGTETLHPQGNP 356

RESULT 3

JC5520

serotonin receptor 6 - human

N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)

C:Species: Homo sapiens (man)

C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999

C:Accession: JC5520

R:Kohen, R.; Metcalf, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.E.; Meltzer, J. Neurochem. 66: 47-56, 1996

A:Title: Cloning, characterization, and chromosomal localization of a human 5-HT 6 serot

A:Reference number: JC5520; MUID:96102917

A:Accession: JC5520

A:Molecule type: mRNA

A:Residues: 1-440 <KOH>

A:Cross-references: GB:L41147; NID:g1162923; PIDN:AA92622.1; PID:g1162924

A:Experimental source: brain

C:Comment: This protein shows high affinity for several therapeutically important ant

C:Genetics:

A:Gene: HTR6

A:Map position: 1p35-36

A:Introns: 238/3; 291/3

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:28-51/Domain: transmembrane #status predicted <TM1>

F:65-88/Domain: transmembrane #status predicted <TM2>

F:100-123/Domain: transmembrane #status predicted <TM3>

F:143-166/Domain: transmembrane #status predicted <TM4>

F:185-208/Domain: transmembrane #status predicted <TM5>

F:266-289/Domain: transmembrane #status predicted <TM6>

F:298-321/Domain: transmembrane #status predicted <TM7>

F:10/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 349.5; DB 2; Length 440;

Best Local Similarity 30.7%; Pred. No. 1e-20;

Matches 127; Conservative 59; Mismatches 171; Indels 57; Gaps 18;

19 VPOTPGSTASGVEVGLRDVASES---VALPFMLLDLTAAGNAVAIVAKTPALR 74

Db 2 VPE-PGP-TNSTPRAMKAGPPSAPGSGWVAALCVIALTA--AANSLLIALICTOPALR 58

75 KE--VEVPHLCVLDLALTLPLAMSSALFPHALFGEVACRLVFLVCFVSLAIS 132

Db 59 NTSNFFLVSLFTSDLMGLVMPAML--NALYGRVVLARGLCLTLVAFDMCCSASILN 116

133 VSAINVERVYVVPMBRYEVRMTGLVAVSYGVVWVVALMAASVPLVGRVSMEE---GAP 189

Db 117 LCLISLDRTLLLSPLRKLMPLRALALVGLWMSLAALASFLPLZ--IGMELGARPP 174

190 SVPPGCSLQMSHAYCOLFVVVFAVLYFLPLLLILLVVCSMFRAVAAMOHGRLPTW 249

Db 175 PVPQCRILASLP-----FVLVAGLFLFPLSGAICFYCYRIILAKKQAVQVSLTGM 229

250 -----ETPROSSESLSRSTWTSAGAQTTPHRTFGGKAAYVLLAVGGFL 298

Db 230 ASQASETLQVPRTPPGESASRLATKHSKAL-----KASLTGLIGLMFV 279

299 CMLPFSPHLVALSAQPISTGQVESVWTWIGYCFSPNPFYGCILNRQIRGELSKQFVC 358

Db 280 TWLPFFVANIYQAV--CCISISGLFD-VLTWIGYCNSTNPIYFLPMDRFRALGR---- 333

359 FFKPAPEELRLP--SRGSIENFLQFLQGTGCPSESWSRPLPSKQEP 411

Db 334 -FLPCP-----RCPREQASLASPLRLTSHSGPRGLS-LQQLVPLPL--PPSD 379

RESULT 4

A39008

histamine H2 receptor - dog

C:Species: Canis lupus familiaris (dog)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Nov-1999

C:Accession: A39008; A41821

R:Gantz, I.; Schaeffer, M.; DelValle, J.; Logsdon, C.; Campbell, V.; Uhler, M.; Yamad

Proc. Natl. Acad. Sci. U.S.A. 88: 429-433, 1991

A:Title: Molecular cloning of a gene encoding the histamine H2 receptor.

A:Reference number: A39008; MUID:91110543

A:Accession: A39008

A:Molecule type: DNA

A:Residues: 1-359 <GAN>

A:Cross-references: GB:342701; NID:g163951; PIDN:AA85637.1; PID:g163952

A:Comment: The nucleotide sequence described in this paper has been revised; the amino a

submitted to the Protein Sequence Database, March 1992

A:Reference number: A41821

A:Accession: A41821

A:Molecule type: DNA
 A:Residues: 1-359 <GA2>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.1%; Score 349; DB 2; Length 359;
 Best Local Similarity 28.7%; Pred. No. 9,2e-21;
 Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

OY 43 SYALFFMLLLDLTAVAGNAAMAVIAKTPALRKEV--FVPHLCVLDLALTLPLMLSSALFD 100
 DB 22 SVTLTLVLLIITLIT--TIAGNVVVCVAVGLNRLRLSLTNCFFVSLAIDLLGLLVLPF---- 74
 OY 101 SAAFLDHL--FGEVACRLYLFLSVCFVSLAILSVSAINVERYYVYVHPMKRYEVRMTLG 157
 DB 75 -SAFYQLSCRSFGKVFVFCVITSLDMVLCVTAISILNLFMSIDRCVAVDPLRYPLVPLPV 133
 OY 158 LVASVGVVWVVKALMASVVPV-LGRVSWEGAP--SVPGCSLQMSHSAVCOLEVVVFAV 214
 DB 134 RYAVSLVLIWVISITLSFLSHLGWNSRNETSFNHTIPKCKVQVN-----LVYGLVDGL 188
 OY 215 LYFLPLLLILLVYCSMFRVARVAAHQGPLFTMETPRQSESLSSNSTVWTSSGAPQT 274
 DB 189 VFYPLPLVMCTIYYRIFKRIADQAKRIHMGSKRA----- 225
 OY 275 TPHRFFGGGKAAYVLLVAGGQFLCWLPRYFSFLYVALSAQPISTGQVESVYTWIGYCF 334
 DB 226 ----TIGHKATVTLAAVAGAFITICWPFYFVYRGKGDDAINEAEVAVVLMGLVANS 281
 OY 335 TSNPFYGCILNQLNGELSKQVCFKPAPE--EELRLPREGSTEEN 380
 DB 282 ALNPLVLTNLNDRFTAYQQLFRC--RPASHAQETSLRSNSQLARN 327

RESULT 5

JC4120
 histamine H2 receptor - guinea pig
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 24-Nov-1999
 C:Accession: JC4120
 R:Traillfort, E.; Vizanete, M.L.; Tardivel-Lacombe, J.; Soull, E.; Schwartz, J.C.; Ruat, M.
 Biochem. Biophys. Res. Commun. 211, 570-577, 1995
 A:Title: The guinea pig histamine H2 receptor: gene cloning, tissue expression and chrom
 A:Reference number: JC4120; MUID:95314628
 A:Accession: JC4120
 A:Molecule type: DNA
 A:Residues: 1-359 <TRA>
 C:Comment: Histamine, a messenger molecule in cell-to-cell communication, affects its ta
 ly defined receptor subtypes named H1, H2 and H3.
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F:22-45/Domain: transmembrane #status predicted <TM1>
 F:58-81/Domain: transmembrane #status predicted <TM2>
 F:93-113/Domain: transmembrane #status predicted <TM3>
 F:136-157/Domain: transmembrane #status predicted <TM4>
 F:179-204/Domain: transmembrane #status predicted <TM5>
 F:235-226/Domain: transmembrane #status predicted <TM6>
 F:269-289/Domain: transmembrane #status predicted <TM7>
 F:4,162,168/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:221,316/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict
 F:226,357/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

Query Match 14.8%; Score 343; DB 2; Length 359;
 Best Local Similarity 27.0%; Pred. No. 2.8e-20;
 Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKEV--FVPHLCVLDLALTLPLMLSSALFD 106
 DB 25 LIIILLIVVAGNVVVCVAVGLNRLRLSLTNCFFVSLAIDLLGLLVLPF-----SAIQ 79
 OY 107 HAL--FGEVACRLYLFLSVCFVSLAILSVSAINVERYYVYVHPMKRYEVRMTLG 163
 DB 80 LSCKSFSGKVCNITVSLDMVLCVTAISILNLFMSIDRCVAVDPLRYPLVPLVPAVAISL 139

OY 164 VGVWVKALAMASVPLVGRVSWEGAPSVPG-----CSLQMSHSAVCOLEVVVFAVFL 218
 DB 140 VFIWISITLSPLST--HLGWNSRNETSKNDPTIVCKVQVN-----EYGLVDGLVFY 192
 OY 219 LPILLILVYCSMFRVARVAAHQGPLFTMETPRQSESLSSNSTVWTSSGAPQTPHR 278
 DB 193 LPILLIMCTIYFIFRIADQAKRIHMGSKRA----- 225
 OY 279 TFGGKAAYVLLVAGGQFLCWLPRYFSFLYVALSAQPISTGQVESVYTWIGYCF 338
 DB 226 TIREHKATVTLAAVAGAFITICWPFYFVYRGKGDDAVNEVPDVLMLGTAANSALNP 285
 OY 339 PFYGCILNQLNGELSKQVCFKPAPEEELRLP--SEGSTEEVFLQFLOCTGCPSESW 395
 DB 286 ILVYALNDRFTAYQQLFRC-----RLASHNSHETSLRLNNSQ-LNRSQCQEPBRW 334
 OY 396 -VSRPL 400
 DB 335 QEDKPL 340

RESULT 6

JH0449
 histamine H2 receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
 C:Accession: JH0449; I52319
 R:Gantz, I.; Munzert, G.; Tashiro, T.; Schaeffer, M.; Wang, L.; DelValle, J.; Yamada,
 Biochem. Biophys. Res. Commun. 178, 1386-1392, 1991
 A:Title: Molecular cloning of the human histamine H2 receptor.
 A:Reference number: JH0449; MUID:91337087
 A:Accession: JH0449

A:Molecule type: DNA
 A:Residues: 1-359 <GAN>
 A:Cross-references: GB:M64799; NID:g184087; PIDN:AAA58647.1; PID:g184088
 R:Nishi, T.; Koike, T.; Oka, T.; Maeda, M.; Futai, M.
 Biochem. Biophys. Res. Commun. 210, 616-623, 1995
 A:Title: Identification of the promoter region of the human histamine H2-receptor gen
 A:Reference number: I52319; MUID:95275318
 A:Accession: I52319
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: GB:D49783; NID:g728495; PIDN:BA08018.1; PID:g728496
 C:Comment: Histamine is important in the regulation of gastric acid secretion.
 C:Genetics:
 A:Gene: GDB:HRH2
 A:Cross-references: GDB:391259; OMIM:142703
 A:Map position: 5pter-5qter
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:23-44/Domain: transmembrane #status predicted <TM1>
 F:58-81/Domain: transmembrane #status predicted <TM2>
 F:93-114/Domain: transmembrane #status predicted <TM3>
 F:135-159/Domain: transmembrane #status predicted <TM4>
 F:181-204/Domain: transmembrane #status predicted <TM5>
 F:233-258/Domain: transmembrane #status predicted <TM6>
 F:268-289/Domain: transmembrane #status predicted <TM7>

Query Match 14.7%; Score 340; DB 2; Length 359;
 Best Local Similarity 28.0%; Pred. No. 4.9e-20;
 Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKEV--FVPHLCVLDLALTLPLMLSSALFD 106
 DB 25 LAVILLIVVAGNVVVCVAVGLNRLRLSLTNCFFVSLAIDLLGLLVLPF-----SAIQ 79
 OY 107 HAL--FGEVACRLYLFLSVCFVSLAILSVSAINVERYYVYVHPMKRYEVRMTLG 163
 DB 80 LSCKSFSGKVCNITVSLDMVLCVTAISILNLFMSIDRCVAVDPLRYPLVPLVPAVAISL 139
 OY 164 VGVWVKALAMASVPLVGRVSWEGAPSV--VPPGCSLQMSHSAVCOLEVVVFAVFL 220

```
Db 140 VLIWISTSLFSLIHLGWNNSRNETSKGNHTTSKCKVOVN-----EYGLVDGLVTFLP 194
Oy 221 LLLLVVCSMRVARVAVAMOHGRLPTWMEPRQSESLSSNSTWTSAGAPQTPHRTF 280
Db 195 LLIKITTYRIKFKVNDOKKRNHISMKAA-----TI 227
Oy 281 GGGKAAYVLLAVGGQFLCMLPFPSFHLVVALSAOPISITGOVESVVTWIGYFCFTSNPF 340
Db 228 RHHKATVTLAAVGAFTICMPFYAFYRGLRGDDALNEVLEALVLMGVANSLNPL 287
Oy 341 YGCLNRQIRGELSKOPVCFKPAPEEELRLPSREG---SIENFLQ 383
Db 288 YALNRDRFTGYQLFCC-----RLANRNSHKTSLRSNASQ 323

RESULT 7
JN0591
N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C:Accession: JN0591
R:Ruat, M.; Talfort, E.; Arrang, J.M.; Tardivel-Lacombe, J.; Diaz, J.; Leurs, R.; Schw
Biochem. Biophys. Res. Commun. 193, 268-276, 1993
A:Title: A novel rat serotonin (5-HT6) receptor: molecular cloning, localization and st
A:Reference number: JN0591; MUID:93277562
A:Accession: JN0591
A:Molecule type: DNA
A:Residues: 1-436 <RUA>
A:Cross-references: GB:S62043; NID:g385708; PIDN:AMB26908.1; PID:g385709
C:Genetics:
A:Introns: 238/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:29-53/Domain: transmembrane #status predicted <TM>
F:63-84/Domain: transmembrane #status predicted <TM>
F:95-122/Domain: transmembrane #status predicted <TM>
F:141-168/Domain: transmembrane #status predicted <TM>
F:185-213/Domain: transmembrane #status predicted <TM>
F:267-293/Domain: transmembrane #status predicted <TM>
F:297-319/Domain: transmembrane #status predicted <TM>
F:9/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 338.5; DB 2; Length 436;
Best Local Similarity 28.4%; Pred. No. 8.1e-20;
Matches 129; Conservative 58; Mismatches 171; Indels 97; Gaps 20;

Oy 2 ESSPPOSSGNSSTLGRVPQTGPSTAGVPEVGLRDVASEVALFEMLLDLTVAGNA 61
Db 4 EPGPV-----NSST---PAMGPGPPAPG-----GSGVVAALCVIVLTA-AAAS 45
Oy 62 AVMAVIATKPALRKF--VFVPHLCVLDLALTLMLPLAMSSALFDHALFGEVACRYL 119
Db 46 LLIIVLTCPALRNTSNFFLVSLFTSDLVGLVMPPALM--NALYGRVYLAIGLCLMLT 103
Oy 120 FLVSCFVSLAISVAIINERYVYVHPMYREVRMTGLIVASVLYGVWVKALAMASVPL 179
Db 104 AFDVWCSSSILNCLISLDRLYLLISPLRYKLRMTAPRALALIGANSLAALASFLPLL 163
Oy 180 GRVSNEE-GAPSV-PCGSLQMSHAYCOL-----FVVYFAVLFLPLLLILVYCSMF 232
Db 164 -LGHNEHGKARTPAPG-----QCRLASLPFVLVAVSVTFPLSGALCFPTCRIL 212
Oy 233 RVARAANOHGRLPTWM-----ETPRQSESLSSRSTWVTSSCAPQTPHRTFG 281
Db 213 LAARKQAOVAVSLTTGTGQALETLQVPRTPRGMESADSRLATKHSKAL----- 264
Oy 282 GGAAYVLLAVGGQFLCMLPFPSFHLVVALSAOPISITGOVESVVTWIGYFCFTSNPF 341
Db 265 -KASLTGILGMEFVWMLPFFVANIQAV-CDGISGLRP-VLTWIGYCSMNPPIY 320
Oy 342 GCLNRQIRGELSKOPVCFKPAPEEELRLP-----SRGSI 377
```

```
Db 321 PLFMRDFKRALGRFLPCVHCP-PEHRPALPPPCGLTAVPDQASACSRCCILCRLQRI 379
Oy 378 EENFLQFLOGT--GC---PSSEWSRPLPSPKQEP 407
Db 380 QTP-----LQGAPRACSSQPSFCCLERPPGTPRHP 410
```

```
RESULT 8
A53281
beta 3-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A53281; S29808
R:Graneman, J.G.; Lahners, K.N.; Chaudhry, A.
Mol. Pharmacol. 40, 895-899, 1991
A:Title: Molecular cloning and expression of the rat beta 3-adrenergic receptor.
A:Reference number: A53281; MUID:92100057
A:Accession: A53281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <GRA>
A:Cross-references: GB:S73473; NID:g241215; PIDN:AMB20702.1; PID:g241216
A:Note: sequence extracted from NCBI backbone (NCBIN:73473, NCBI:P:73476)
R:Bensaid, M.; Kaghad, M.; Rodriguez, M.; le Fur, G.; Caput, D.
FEBS Lett. 318, 223-226, 1993
A:Title: The rat beta3-adrenergic receptor gene contains an intron.
A:Reference number: S29808; MUID:93178631
A:Accession: S29808
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <BEN>
A:Cross-references: GB:S56481; NID:g298306; PIDN:AMB25520.1; PID:g298307
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
```

```
Query Match 14.5%; Score 337; DB 2; Length 400;
Best Local Similarity 28.2%; Pred. No. 9.7e-20;
Matches 120; Conservative 65; Mismatches 188; Indels 52; Gaps 17;

Oy 4 SPIPOSSGNSSTLGRVQP-TPGPSTAGVPEVGLRDVASEVALFEMLLDLTVAGNA 62
Db 2 APWPKNGSLFWSDAPPLDPSAANTSGLPV-----PMAALAGALLALATVAGML 54
Oy 63 VMAYIAKTPALRKF--VFVPHLCVLDLALTLMLPLAMSSALFDHALFGEVACRYL 120
Db 55 VITALARTPRIQTINNVETSLATADLVGLVMPG--ATLALGHMPLGATGELMTS 112
Oy 121 LSCVCSLAIISVAIINERYVYVHPMYREVRMTGLIVASVLYGVWVKALAMASVPL 180
Db 113 VDVLCTVTAISFTICALAVDRYLAVTNPLRYGLVTKRRARAAYVWLVASATVSFAPIMS 172
Oy 181 RYSWEGAPSVPPGSLQMSHAYCOL-----FVVYFAVLFLPLLLILVYCSMPFVA 235
Db 173 Q-WMRVGADEAQECH---SNPRCCSFASNMPTALSSVSFTYLDLVLMLVYARVYVA 228
Oy 236 ---FVAAMOHGRLPTWMEPR--QRSESLSSRSTWVTSSGAPQ--TTPHR--TFGGGA 285
Db 229 KRQRLRLRELGRPP-DESPRSPSPSPATVGPPTASDGVSCGRPARLLPLGEHRA 287
Oy 286 AVLLAVGGQFLCMLPFPSFHLVVALSAOPISITGOVESVVTWIGYFCFTSNPFYGLN 345
Db 288 LRTLLGILGIFSLCPFLFANVLRALVGPISLVPSGVFTALNWLGYANSAFNPLTY-CRS 346
Oy 346 RQIRGELSKOPVCFKPAPEEELR-----LPSREGSIENFLQFLOGTGCPSSEVVS 397
Db 347 PDER-DARRLDLSYGGNGPEPRVVTTPASBPVASKRNSPLNR-----DGYEGE---- 395
Oy 398 RPLPS 402
Db 396 RPFP 400
```

RESULT 9

A1679

beta-3-adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 13-Aug-1999

C:Accession: A1679

R:Muzlin, P.; Revelli, J.P.; Kuhn, F.; Cocayne, J.D.; McCombie, W.R.; Ventler, J.C.; Gia

R: Biol. Chem. 266, 24053-24058, 1991

A:Title: An adipose tissue-specific beta-adrenergic receptor. Molecular cloning and down

A:Reference number: A1679; MUID:92084710

A:Accession: A1679

A:Molecule type: mRNA

A:Residues: 1-400 <MU2>

A:Cross-references: GB:M74716; NID:9950087; PIDN:AAA4470.1; PID:g202766

A:Experimental source: brown adipose tissue

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 336; DB 2; Length 400;

Best Local Similarity 28.2%; Pred. No. 1.2e-19;

Matches 120; Conservative 64; Mismatches 189; Indels 52; Gaps 17;

QY 4 SPIQSSGNSSTLGRVPO--TPGPSTASGVPEYGLRDVASESVAFPFMLLDLTAVAGNNA 62

Db 2 APWPHKNSLAFWSDAPFLDPSAANTSGPGV-----PMAALAGALLALATVGNML 54

QY 63 VMAVIAKTPALRK--VVVFHLCIVDLAALTPLMLSSALFDHALFGEACRYLFE 120

Db 55 VITALARTPRLOTITNVFVTSLATADLVVGLVMPG--ATLALGHPMLGTCGLWTS 112

QY 121 LSVCFVSLAISVSAINVERYYVHPMKREYRMTGLVASVYGVWVKALMAASVPVIG 180

Db 113 VDVLCTVSIETLCLAVDRILATNPRLTGTLTKRRARAIVLVWVYSAVSPATIMS 172

QY 181 RVSMEGAPSVPPGCSLQMSHAYCOL-----FVVFAVLVFLDLLILVYCSMFYA 235

Db 173 Q-WMVVGADAEAGQCH---SNRCCSFASNMRYALLSSVSRYLPLVLMFYAAVFYA 228

QY 236 ---RVAAMOHGPLETMMETPR--ORSELSRSSTWVTSSGAP--TTPHR--TFGGGKA 285

Db 229 KRORFVRELRGPRP--EESPRSPSPSPATVGTPTASDGVSCRRPARLLPGEHRA 287

QY 286 AVLLAVGGOFLLCWLPRFSEFHLVYALSAOPISITGVESVWVWIGYFCFTSPFFYGLN 345

Db 288 LRTGLIGTISLCLWLPFLAVLALVPSLVPSGVFTALWLVGANSAPFLIY-CRS 346

QY 346 ROIRGELSKQVCFKPAPEEELR-----LPSREGSIEENFLQFLOGTCPSSESWVS 397

Db 347 PDFR-DARRRLICSGGSGPEPRVYVTFPASPVASRQNSPLNRF-----DQYEGE--- 395

QY 398 RPLPS 402

Db 396 RPFPT 400

RESULT 10

S65459

beta-3-adrenergic receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999

C:Accession: S65459

R:Pietri-Rouxel, F.; Lenz, G.; Kpooor, A.; Dymare, M.F.; Archimbault, P.; Strosberg,

Eur. J. Biochem. 230, 350-358, 1995

A:Title: Molecular cloning and pharmacological characterization of the bovine beta3-adre

A:Reference number: S65459; MUID:95324546

A:Accession: S65459

A:Molecule type: mRNA

A:Residues: 1-405 <PIE>

A:Cross-references: EMBL:X85961; NID:9757758; PIDN:CAAS9937.1; PID:9757759

A:Experimental source: brown adipose tissue

R:Castella, L.; Muzlin, P.; Revelli, J.P.; Riquier, D.; Giacobino, J.P.

Biochem. J. 297, 93-97, 1994

A:Title: Expression of beta(1) - and beta(3) -adrenergic-receptor messages and adenylat

ite fat.

A:Reference number: S40503; MUID:94107292

A:Accession: S40504

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 162-298 <CAS>

R:Stoffel, B.; Meyer, H.H.D.

submitted to the EMBL Data Library, June 1992

A:Description: Bovine beta3-adrenergic receptor, partial genomic sequence.

A:Reference number: S31659

A:Accession: S31659

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 4-5, 'HE', 8-105 <STO>

A:Cross-references: EMBL:X67214

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:37-63/Domain: transmembrane #status predicted <TM2>

F:73-101/Domain: transmembrane #status predicted <TM1>

F:113-133/Domain: transmembrane #status predicted <TM3>

F:156-179/Domain: transmembrane #status predicted <TM4>

F:204-225/Domain: transmembrane #status predicted <TM5>

F:293-314/Domain: transmembrane #status predicted <TM6>

F:327-347/Domain: transmembrane #status predicted <TM7>

F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 335.5; DB 2; Length 405;

Best Local Similarity 28.1%; Pred. No. 1.3e-19;

Matches 121; Conservative 67; Mismatches 183; Indels 59; Gaps 18;

QY 7 PQSSGNSSTLGRVPTP--GPST--ASGVPEGLRDVASESVAFPFMLLDLTAVAGNNA 62

Db 3 PWPBNGSS-LTPWPDIPFLAPRTANASGIPGW----AVALAGALLALATVATVGNML 57

QY 63 VMAVIAKTPALRK--VVVFHLCIVDLAALTPLMLSSALFDHALFGEACRYLFE 120

Db 58 VITALARTPRLOTITNVFVTSLATADLVVGLVMPG--ATLALGHPMLGTCGLWTS 115

QY 121 LSVCFVSLAISVSAINVERYYVHPMKREYRMTGLVASVYGVWVKALMAASVPVIG 180

Db 116 VDVLCTVSIETLCLAVDRILATNPRLTGTLTKRRARAIVLVWVYSAVSPATIMS 175

QY 181 RVSMEGAPSVPPGCSLQMSHAYCOL-----FVVFAVLVFLDLLILVYCSMFYA 235

Db 176 K-WMIRIGADAEAGQCH---SNRCCSFASNMRYALLSSVSRYLPLVLMFYAAVFYA 231

QY 236 ---RVAAMOHGPLETMMETPR--ORSELSRSSTWVTSSGAP--TTPHRTFGGG 283

Db 232 TRORLRLRELGRFPPESSPAPRSRSGSLAGPACASVAGVSYRRARLLPAREH--- 288

QY 284 KAAVLLAVGGOFLLCWLPRFSEFHLVYALSAOPISITGVESVWVWIGYFCFTSPFFYGC 343

Db 289 RALRTGLIGTISLCLWLPFLAVLALVPSLVPSGVFTALWLVGANSAPFLIY-C 347

QY 344 LNRQIRGELSKQVCFKPAPEEELR--PSREGSIEENFLQFLOGTCPSSESWSRPL 401

Db 348 RSPDFRSAP-RRLIC--RCRPEHLAASPPR-----APSGAPALTATSP 388

QY 402 SPKQEPFPAVD 411

Db 389 AGPMQPPELD 398

RESULT 11

A55044

beta-4C-adrenergic receptor - turkey

C:Species: Meleagris gallopavo (common turkey)

C:Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C:Accession: A55044

R:Chen, X.; Harden, T.K.; Nicholas, R.A.

J. Biol. Chem. 269, 24810-24819, 1994

A:Title: Molecular cloning and characterization of a novel beta-adrenergic receptor.

A:Reference number: A55044; MUID:95014249
A:Accession: A55044
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <CH>
A:Cross-references: GB:U1378; NID:g555881; PIDN:AAA62151.1; PID:g555882
C:Genetics:
A:Introns: 416/2
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match 14.5%; Score 335; DB 2; Length 428;
Best Local Similarity 27.3%; Pred. No.1.5e-19;
Matches 115; Conservative 59; Mismatches 179; Indels 68; Gaps 15;

OY 22 TPGSPSTASVPEVGRLDVASESVALEFFMILLD-LTAVAGNAVMAMVIKTPALRKFL--VF 78
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 2 TPLPFGNGSVPCSNAAVLTSRQWAVGAALSTITLVIVAGNLIVAIKAFTPLRLOTMTNF 61

OY 79 VFHLCLVDLLALTLPMLAMLSLAFDHALFGEVACRYLFYSVCFSLATISVAINV 138
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 62 VTLACADLVKLVLVPPG--ATILLSGHMPGYVCWEMLTSLDLVLTCTASTETLCATAIV 119

OY 139 ERTYYVHPMRREVRNTGLVASVLGVVAKALMAVPVLCRGVMBEGAPSPGCCSLQ 198
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 120 DRYLTITAPLOYEALVTIKRAMAVVCMWAISAFISPTIKNH-WMRGDADQAVRC--- 175

OY 199 WSHSAVCOI-----FVVGFVAVLYFLPLLILVYCSMFRA-----RVANOHG 243
DB 176 YDDPRCCDEPTMTYAIVSYTFYVPLLMTFEVYVRFAVATRNVQLGRKKVFLQEN 235

OY 244 PLPTMETPTPROSESLSRSSTWTSSGAPQTTPHTFC--GGKAAYVLANGQFLCWL 301
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 236 P-----SLSSR-----GGRWRPRSLLAIKEHKAKTKIGTINGFTFLCWL 275

OY 302 PFESHLVVALAOPRTSQVESVTTWIGYFCFTSNPFYCGCLNQINGELSKOEVCFEK 361
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 276 PRFVANIT-IKVCRPLVPQQLFLPLNMLCYVNSAARNPIIT-CRSDPFRSAFKLLCC--- 330

OY 362 PAPEBELRLPSREGSIENEFLQFLTQGTCPSESWSRPLSPKQEPBPVDFRIPOQIAEE 421
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 331 -----PRADRRLHAAPQDPQHSC----AFSPGCDPMEDSKAVD---PGLHRED 373

OY 422 T 422
:
DB 374 S 374

RESULT 12
139369
alpha-1a-adrenergic receptor - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
C:Accession: 139369; JC2331
R:Espenhader, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Mineman, K.P.; R
M.I. Pharmacol. 47, 977-985, 1995
A>Title: Cloning of the human alpha 1a-adrenergic receptor and inducible expression of t
A:Reference number: 139369; MUID:95265059
A:Accession: 139369
A>Status: preliminary; translated from GR/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-572 <RES>
A:Cross-references: NID:g914933; PIDN:BAH06222.1; PID:g914934
R:Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A>Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A:Reference number: JC2331; MUID:94296402
A:Accession: JC2331
A:Molecule type: mRNA
A:Residues: 1-30,'G','32-521,'P','523-572 <WEI>
A>Note: The authors translated the codon CCC for residue 522 as Arg
C:Genetics:
A:Gene: GDB:ADRA1A; ADRA1; ADRAIR

A:Cross-references: GB#118749; OMIM:104229
A:Map position: 20pter-20qter

A:Introns: 37/3
C:Superfamily: vertebrate rhodopsin
G:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F.89-123/Domain: transmembrane #status predicted <TM1>
F.132-167/Domain: transmembrane #status predicted <TM2>
F.172-197/Domain: transmembrane #status predicted <TM3>
F.208-235/Domain: transmembrane #status predicted <TM4>
F.254-278/Domain: transmembrane #status predicted <TM5>
F.344-374/Domain: transmembrane #status predicted <TM6>
F.380-414/Domain: transmembrane #status predicted <TM7>
F.65;82/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 14.3% Score 332.5; DB 2; Length 572;
Best Local Similarity 24.2%; Pred. No. 3,3e-19;
Matches 122; Conservative 77; Mismatches 204; Indels 101; Gaps 16;

DQ 12 NSSLTGRVQTGPSPASGVPEGLRDVASESVAL-FEMILLDTITAVAGNAAMVIARTK 70
 : | | | |
Db 65 NNSSAGEPSSAGSGDVNCTAAVGILVSAQGVCVFLLAAFLTMAVGNLIVLSACN 124
 ||| | | | |
DQ 71 PALRKTV--FWHCLLVLDLAALTPLMLSSALFDHALREVAACRLYLPISCVSL 128
 | | | | |
Db 125 RHLQVTNYFYINLAADVADLLSATVLPSF--ATMEVLGFMAFGRAFCDDWAAVDLCCTA 182
 ||| | | | |
OY 129 ALLSVSAIINVERYYYVHHMRYEVRMTLGIVASVLGVVVKKALAMASVPYLGRVSMEGA 188
 |||| | | | |
Db 183 SLTSICTISVDRTVGYRHSCLKTPAIINTERKAAILALLMWVALLVSVGPLG--WKE-- 237
 ||| | | | |
OY 189 PSYPPECSSLQWSHSAVCQL-----FYVFAVLTYPLLILLYVYSMSRVAR--VAAMO 241
 ||| | | | |
Db 238 -PVPP-----DERPCGITTEAGYAVFSSECFYIPMAVIYMYCRYVVAVSTRRSLE 289
 ||| | | | |
OY 242 HGPLPTWMETPRORSES-----LSSRSYMVNSSGA--POTPHRFPGGG----- 283
 ||| | | | |
Db 290 AG-----VKERCKASEVLRIRHRCGAATGADGHNCRSKAGHTFRSSLSVRLLKFSR 342
 ||| | | | |
OY 284 --KAAVLLLAGGOELLCLPYPFSEHLVYALSQAPISTQOVESVTWIGFCTSNPFY 341
 ||| | | | |
Db 343 EKAKAATTTLIAVGVEFLCMFPFEFFVLPLGSIFPOLKPSGEVFVFIWLGYFNSCVNPLAY 402
 ||| | | | |
OY 342 GCNLRIIRELSNQFVCFK-----PAPEELRLPSRGSIENLENLOFL 385
 ||| | | | |
Db 403 PSSSRFFKAFLLRLCCQRRRRRRPRLMKRYGHMRASTISGLROCAFS----- 453
 ||| | | | |
OY 386 QGTGCPSSESWSNRLPSPKOEPPAV-----DFRIPOIAIBETSFPLE 427
 ||| | | | |
Db 454 -GDAPGADLALITALPDDEPPCPREMQAIVASRRKPSPAFREWRLLGFFRRPTT---- 508
 ||| | | | |
OY 428 QOLTSDIIMSDSLRLPASPRLES 451
 ||| | | | |
Db 509 -QLRAKVSSLSHKRIRAGAORAFA 531

RESULT 13
157942
5-hydroxytryptamine receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I57942
R.Monsma, F.J.
Mol. Pharmacol. 43, 320-327, 1993
A>Title: Cloning and expression of a novel serotonin receptor with high affinity for
A:Reference number: I57942; MWID:I93196808
A:Accession: I57942
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-437 <RES>
A:Cross-references: GB:I03202; NID:g294507; PID:NAAA0618.1; PTD:g294508
C:Superfamily: Vertebrate Rhodopsin

Query Match 14.2% Score 329.5; DB 2; Length 437;

F:1-402/Product: beta-3-adrenergic receptor precursor splice form 1 #status predicted <M
F:37-63/Domain: transmembrane #status predicted <TM1>
F:73-101/Domain: transmembrane #status predicted <TM2>
F:113-133/Domain: transmembrane #status predicted <TM3>
F:156-178/Domain: transmembrane #status predicted <TM4>
F:204-225/Domain: transmembrane #status predicted <TM5>
F:293-314/Domain: transmembrane #status predicted <TM6>
F:327-347/Domain: transmembrane #status predicted <TM7>
F:8,26/Blinding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.0%; Score 324; DB 1; Length 414;

Best Local Similarity 28.7%; Pred. No. 1.le-18;

Matches 125; Conservative 63; Mismatches 187; Indels 60; Gaps 21;

QY 4 SPIQSSGSSSTLGRVPP--GPSA--SGVEYGLRDVASESVAFMLLDLTAVAG 59
DB 2 ARMPH---ENSSLAMPDLPTLPTANTSGLPVPW---EALAGALLALAVLATVGG 54
QY 60 NAAVAVIAKTPALRK--VEVHLCVLDLALTLMLPLMLSSALFDPHALGEVACRL 117
DB 55 NLVIVAIAMTPTRLQTMVTFVTSIAADLVGMLVPPA--ATLALTGHPMLGATGCEL 112
QY 118 YFLSVCEYSIALISVSAINVERIYVHPMYEVAMTIGLVA SVLVGVYKALAMASVP 177
DB 113 WTSVVLCTASIEITLCALAVDRYLAVTNPLRYGALVTRCARAVLVWVSAVSEFAP 172
QY 178 VLGRVSMEEGASVPPGCSLQMSHAYCOL---FVVVEAVLYFLPLLLILVYCSMF 232
DB 173 IMSQ--WMRGALAEORCH---SNPRCCAFASNMRYLLSSVSFTPLLVMLFYIARVF 228
QY 233 RVA---RVAAMQHGPPLPTMETPRORSESLSR--STWVTSSGAP-----QTTPHRT 279
DB 229 VVATRLRLRLRGELGRFP--EESPAPSRSLAPAPVGTCAPEGVACGRPARLLPRE 287
QY 280 FCGGKAAYVLLVAGGOFLLCMLPYFSFLVYALSAPITGQVESVYTWIGYFCFTSNPF 339
DB 288 H--RALCTGLIMGTFTLCMLPFLANVLRALGSPSLVPGPAFLALNMLGYANSAFNPL 344
QY 340 FYGCLNROIIGELSKQFVC---FFKPAPEELR---LPS-----REGSIENFLOFLOG 387
DB 345 IY-CRSPDERSAF--RRLCRRCGRRLPPEPCAAARPALFPSSGVPARSSPAOPRLCORLDG 402
QY 388 -TGCPSESWSRPLP 401
DB 403 FDSGCGEN---PLP 413

Search completed: October 21, 2002, 16:08:41

Job time : 23 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:11 : Search time 14 Seconds

(without alignments)
1247.323 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318
Sequence: 1 MESSPIPOSSGNSSTIGRP.....SDIIMSDSYLRPASPRLES 451.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	823	35.5	428	1	GPX1178 Oryzias lat
2	351	15.1	428	1	GPX1178 Oryzias lat
3	349.5	15.1	440	1	GPX1178 Oryzias lat
4	349	15.1	359	1	GPX1178 Oryzias lat
5	345	14.9	358	1	GPX1178 Oryzias lat
6	344	14.9	358	1	GPX1178 Oryzias lat
7	344	14.8	359	1	GPX1178 Oryzias lat
8	343	14.8	359	1	GPX1178 Oryzias lat
9	340	14.7	359	1	GPX1178 Oryzias lat
10	338.5	14.6	436	1	GPX1178 Oryzias lat
11	337	14.5	400	1	GPX1178 Oryzias lat
12	335.5	14.5	405	1	GPX1178 Oryzias lat
13	335.5	14.5	405	1	GPX1178 Oryzias lat
14	335	14.5	428	1	GPX1178 Oryzias lat
15	332.5	14.3	572	1	GPX1178 Oryzias lat
16	326.5	14.1	400	1	GPX1178 Oryzias lat
17	323.5	14.0	405	1	GPX1178 Oryzias lat
18	322.5	13.9	418	1	GPX1178 Oryzias lat
19	321.5	13.9	398	1	GPX1178 Oryzias lat
20	321.5	13.9	405	1	GPX1178 Oryzias lat
21	320.5	13.8	562	1	GPX1178 Oryzias lat
22	319.5	13.8	408	1	GPX1178 Oryzias lat
23	317.5	13.7	379	1	GPX1178 Oryzias lat
24	315	13.6	351	1	GPX1178 Oryzias lat
25	312.5	13.5	405	1	GPX1178 Oryzias lat
26	306.5	13.2	519	1	GPX1178 Oryzias lat
27	305	13.2	515	1	GPX1178 Oryzias lat
28	301	13.0	515	1	GPX1178 Oryzias lat
29	300.5	13.0	466	1	GPX1178 Oryzias lat
30	300	12.9	466	1	GPX1178 Oryzias lat
31	299.5	12.9	539	1	GPX1178 Oryzias lat
32	298.5	12.9	466	1	GPX1178 Oryzias lat
33	295.5	12.7	514	1	GPX1178 Oryzias lat

34	293.5	12.7	478	1	OPN4_HUMAN	Og9uh6 homo sapien
35	292	12.6	466	1	ALIA_RAT	P43140 rattus norv
36	291.5	12.6	388	1	SH4_HUMAN	Q13639 homo sapien
37	291	12.6	470	1	ALIA_ORYLA	Q91175 Oryzias lat
38	290.5	12.5	501	1	YONJ_CABEL	O02213 caenorhabdi
39	290	12.5	466	1	ALIA_BOVIN	P18130 bos taurus
40	289.5	12.5	388	1	SSR4_HUMAN	P11391 homo sapien
41	289	12.5	446	1	DADR_MACMU	O77680 macaca mula
42	288	12.4	452	1	A2AA_BOVIN	Q28838 bos taurus
43	286.5	12.4	388	1	SH4_CAVPO	O70528 cavia porce
44	285.5	12.3	564	1	SH41_DROME	P20905 drosophila
45	285	12.3	446	1	DADR_HUMAN	P21728 homo sapien

ALIGNMENTS

RESULT 1	ID	GPX1178	STANDARD	PRT	428 AA
AC	GPX1178				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	Probable G protein-coupled receptor (Fragment).				
OS	Oryzias latipes (Medaka fish).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;				
OC	Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.				
ON	NCBI_TaxID=8090;				
RX	SEQUENCE FROM N.A.				
RA	MEDLINE-95275927; PubMed-7756357;				
RA	Yasuda A., Abe K., Saigo K., Arai S., Emori Y.;				
RT	"Molecular cloning of a fish gene encoding a novel				
RT	seven-transmembrane receptor related distantly to catecholamine,				
RT	histamine, and serotonin receptors.";				
RL	Biochim. Biophys. Acta 1235:467-469(1995).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: DA3633; BAA07741.1; -.				
DR	GCRDB: GCR_1566; -.				
DR	InterPro: IPR00276; GPCR_Rhodpsn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.				
DR	PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN	1	46		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	47	67		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	68	93		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	94	114		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	115	120		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	121	141		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	142	162		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	163	183		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	184	210		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	211	231		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	232	293		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	294	314		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	315	>428		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	395	398		EXTRACELLULAR (POTENTIAL).
FT	CARBOHYD	18	18		POLY-SER.
FT	NON_TER	428	428		N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 428 AA; 47359 MW; B749E8765B58A38F CRC64;

Query Match 35.5%; Score 823; DB 1; Length 428;
Best Local Similarity 42.3%, Pred. No. 1.le-44;
Matches 184; Conservative 81; Mismatches 142; Indels 28; Gaps 11;

OY 2 ESSPI---POSSGNAST--LGRVPTPGSPSTASGVPEVL-----RDVASSEVALFEFMILL 52
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 5 KTSPIITSDHSTLSNFTSTGLFGPHVP-----PDVGVTSSOSQMKDLFGLCWYTL 56
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 53 DLTAVGNAVAVAVIATKTPALRKFEVFPHCLVDLLAALTLPMLASSSALFDHALPGE 112
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 57 NLIALANTGMVVVALARAPHLKKFAFYCHLCADVLCALILMPGLTISSPPFGVVFPI 116
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 113 VACRLYLELSCFVSVALISVAINVERYYVHPMRKEVRMTGLVASLVGVWKALA 172
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 117 LECQYIEFLNFLEMLILTITTAIVEREFYIVHPMRKEVKMTINLVIGVMILLMFKSLL 176
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 173 MASVPVLCRVSEDEAPSVPRGCCSLQMSHSANCOLFVVVFAYVLPLPLLTLVVYCSHF 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 177 LALVTLFGPPRGHOSSIAASHCSLHASISRLRGVFALEVCICELAPVVFYSAYV 236
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 233 RVARYAAHQHG-P-LPTMMET--PRORESLSRSRMVTSAGAPQ--TTPRTFGGKAAYV 288
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 237 KVARSNALAQVPAVYPTMADASPARKDSINSQTIIITRTLPLQRSLPERASGGKALIT 296
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 289 LLAVGGQELLCLPYFSFHLVVALSAOPISTGOVESVYTWIGFCFTSNPFYGGCLNRQI 348
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 297 LAFIYGOFVLCVLPFFIFLOXSLTGSMKSPDLEAEVAMVLAYSFAVPNSFYGLLNROI 356
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 349 RGELSK-QVCFCKRAPEELLPREGSIENFIQLQFLQGTCGPSESWSRPLSPK-QE 406
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 357 RDELVKFRCCCTQTPV---EIGPSLSLEGSEFNLFQIORTSSSETHPFSANSRNME 413
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 407 PPVADFPRIQGAEE 421
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 414 NQA-HKITPGQIP EE 426
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2
HH2R-RAT STANDARD: PRT: 358 AA.

ID HH2R-RAT
AC P25102.1 MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histamine H2 receptor (H2R) (gastric receptor I).
GN HRH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
MEDLINE=92028890; PubMed=1930188;
RA Rust M., Traifort E., Arrang J.-M., Leurs R., Schwartz J.-C.;
RT "Cloning and tissue expression of a rat histamine H2-receptor gene.";
RL Blochem. Biophys. Res. Commun. 179:1470-1478(1991).
CC -! FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
CC -! SIMILARITY: BELONGS TO INTEGRAL MEMBRANE PROTEIN.
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL; S57565; AAB19935.1; .

[illegible]

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Best Local Similarity 30.7%, Pred. No. 3.5e-15;
Matches 127; Conservative 59; Mismatches 171; Indels 57; Gaps 18;

OY 19 VPQTPGSTAGVPEVGLRDVASES-----VALFFMLLDLTPAVAGNAVMVAIAKTPALR 74
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 VPE-PGP-TANSTPAMGAGPPSPAGSGCWMAALCVYIALTR-AANSLILALICQPALR 58
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 75 KF--VFVEFHLCVLDLALATLPLMLAMSSSALFDHALFEVACRLYLFSVCFVSLAIS 132
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 NTSNFFELVSLFTSDMLGVMPAMPAL--NALYGRWVLYARGCLLMTAFDWCSCASITLN 116
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 133 VSAIVVEEYVYVHMKREVRRTGLVASVGVVKAALMAASVPLGRVSMEE---GAP 189
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 LCLISLDRLYLISPLRKRLRMTPLRALATLVGAWSIALAALSFLPL--LGMHEHGHARP 174
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 190 SVPPGCSLOWMSHAQCOLFEVYVFAVLYFLPLLLILVYCGSMFRAVARAAOHGDLPTWM 249
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 PVPGGCRLIASLP-----FVLVASGLTFPLPSGALCFYTCRIILAAKQAQVVASLTIGM 229
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 250 -----ETPRORSESLSSRSTWVTSQAPQTPPHRTFGGKAAYVLLAVGQPL 298
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 230 ASQASGETLQVPRTPRGVEASADSRRLATKHSKAL-----KASLTGLIGLMFEV 279
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 299 CWLPPEFHLVYALSAQIPISTGVESVVTWYIGFECTSNPFYGLNQINGELSKQVVC 358
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 280 TWLPPEFVANIYQAV-CDCISPLGLP-VLTWLTGVCSTNNPIIYPLFMDQFRLALGR---- 333
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 359 FFKPAPREBELRLP-SREGSIEENFLQILOGNGCPSESWVRPLSPKQEPAYD 411
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 334 -FLPP-----KCPREKQASLASPSLRITSHSGPRPOLSLQQVLPPLP--PPDSD 379
   ||: ||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
HH2R_CANFA
ID ID HH2R_CANFA STANDARD: PRT: 359 AA.
AC P17124:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histamine H2 receptor (H2R) (Gastric receptor 1).
GN HHR2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91110543; Pubmed=1703298;
RA Gantz I., Schaeffer M., Delvalle J., Logsdon C., Campbell V.,
RA Uhler M., Yamada T.;
RT "Molecular cloning of a gene encoding the histamine H2 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:429-433(1991).
RN [2]
RP MUTAGENESIS OF HISTAMINE-BINDING RESIDUES.
RX MEDLINE=93015991; Pubmed=1356984;
RA Gantz I., Delvalle J., Wang L.-D., Tashiro T., Munzert G., Guo Y.-J.,
RA Konda Y., Yamada T.;
RT "Molecular basis for the interaction of histamine with the histamine
H2 receptor.";
RL Biol. Chem. 267:20840-20843(1992).
RL -I- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: GASTRIC FUNDUS AND, TO A LESSER EXTENT, IN
CC BRAIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR EMBL: M32701: AAA85637.1; .
DR PTR: A39008: A39008.
DR HSSP: P29274: 1MMH.
DR GCRdb: GCR_0014: .
DR InterPro: IPR000276: GPCR_Rhodopsn.
DR Pfam: PF00001: 7tm_1; 1.
DR PRINTS: PS00237: GPCR_Rhodopsn.
DR PROSITE: PS50262: G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262: G-PROTEIN_RECEP_FL_2; 1.
KW G-Protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22
FT TRANSSEM 23 44
FT TRANSSEM 45 57
FT TRANSSEM 58 81
FT TRANSSEM 82 92
FT TRANSSEM 93 114
FT TRANSSEM 115 134
FT TRANSSEM 135 159
FT TRANSSEM 160 180
FT TRANSSEM 181 204
FT TRANSSEM 205 234
FT TRANSSEM 235 258
FT TRANSSEM 259 267
FT TRANSSEM 268 289
FT TRANSSEM 290 359
FT SITE 98 98
FT SITE 186 186
FT SITE 190 190
FT CARBOHYD 4 4
FT DISULFID 91 174
FT MUTAGEN 98 98
FT MUTAGEN 186 186
FT MUTAGEN 190 190
FT MUTAGEN 190 190
SQ SEQUENCE 359 AA; 40201 MW; 37E36412DF58B805 CRC64;
Query Match 15.1%; Score 349; DB 1; Length 359;
Best Local Similarity 28.7%; Pred. No. 3,2e-15;
Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

OY 43 SVALEFMLLDLTAVAGNAVAIAKTPALRKV--FVFHLCVLDLAALTLMLAMLS 100
DB 22 SVLVTLVLI---TAGVNVVCLAVGLNRRLSLNCFIVSLAITDILGLLVLPF---- 74
OY 101 SSALFDHAL---FGEVACRLVLFVSCFVSLAIVSAINERYVVVHPREYVRMTLG 157
DB 75 -SAFYQLSCRMFSFGKVFENITSTLDVLMCTASILNLFMISIDRCAYVDPLKYPVLTPV 133
OY 158 LVASLVGVWVKALAMASVVP--LGRVSWDEGAP--SVPPGSLQWSHAYCOLFVVVFAV 214
DB 134 RVAASLVLIWVISTLSLSTLSLHGWNSRNETSSFNHTIPKCVQVN---LVYGLVGL 188
OY 215 LVFLPLLLILVVVCSMRVARVAMOHGRLPTWMTETPROSESLSSRSTWTSAGAPOT 274
DB 189 VTFYPLLVLMCTTYRIKRIARDQAKRIHHGSKAA----- 225
OY 275 TPHTFGGKAAYVLLAVGOFLLCWLPRYFSFHLVALSAOPISIGOVESVVTWIGYFCF 334
DB 226 ---TIGEHKATVTLAAVGAFTICMPFYFVYVYRGKGDGDAINEAEVAVVLMGYANS 281
OY 335 TSNPFYCGLNKQINGELSKQVCFKPAPE--BELRLPSREGSTEEN 380
DB 282 ALNPILYATLNRDFTAYQOLFRC--RPAASHAQETSLRSNSSQLARN 327

AC P97292;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histamine H2 receptor (H2R) (Gastric receptor I).
GN HRH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA;
RX MEDLINE=97092891; PubMed=8938453;
RA Kobayashi T., Inoue I., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RT Watanabe T.;
RT "Cloning, RNA expression, and chromosomal location of a mouse
histamine H2 receptor gene";
RL Genomics 37:390-394(1996).
CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL: D50096: BAA08792.1; .
DR GCRdb: GCR_1155: .
DR MGD: MGI:108482: Hrh2.
DR InterPro: IPR000276: GPCR_Rhodopsn.
DR Pfam: PF00001: 7tm_1; 1.
DR PRINTS: PS00237: GPCR_Rhodopsn.
DR PROSITE: PS00237: G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262: G-PROTEIN_RECEP_FL_2; 1.
KW G-Protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22
FT TRANSSEM 23 44
FT TRANSSEM 45 57
FT TRANSSEM 58 81
FT TRANSSEM 82 92
FT TRANSSEM 93 114
FT TRANSSEM 115 134
FT TRANSSEM 135 159
FT TRANSSEM 160 179
FT TRANSSEM 180 203
FT TRANSSEM 204 233
FT TRANSSEM 234 257
FT TRANSSEM 258 266
FT TRANSSEM 267 288
FT TRANSSEM 289 358
FT DOMAIN 98 98
FT SITE 185 185
FT SITE 189 189
FT SITE 189 189
FT CARBOHYD 4 4
FT DISULFID 91 173
FT SEQUENCE 358 AA; 40379 MW; D3DBA81D1B6D927 CRC64;
Query Match 14.9%; Score 345; DB 1; Length 358;
Best Local Similarity 27.6%; Pred. No. 5,6e-15;
Matches 108; Conservative 58; Mismatches 153; Indels 74; Gaps 12;

OY 42 ESVALEFMLLDLT---AVAGNAVAIAKTPALRKV--FVFHLCVLDLAALTLML 94

Db 13 DSALKVTSVLTFTLPIITVAGNVVCLAVSLNRRLSLNCFIVSLAATDILLGLVM 72
QY 95 PLAMISSALDHAL---FGEVACRLYLFLSVCPVSLAITSVAINVRYYVHPMKRE 151
Db 73 PF---SAIQLSFKMFGGVFCNITYTSLDMCTASILNLFMTSLDRYCAVDDPLKXP 127
QY 152 VRMTGLVASVYGVVWVMAVAVPVVGRVSWEE-----GAPSVPGCSLQMSHSAVC 205
Db 128 VLVPVRAVIAISVFIWVISTLSLST---HIGMNSRNTKRGNDTFK--CKVQVN----- 178
QY 206 QLFVVFVAVLYLLPLLLILVYVCSMPFRAVAAQHPLEPTMPRORSESLSRSTM 265
Db 179 EYGVLDGMVTFYLLPLIMCTVYTRIFKIAREQAKRINHISMKAA----- 224
QY 266 VTSSGAQPTTHRTFFGGKAAVVLAVGQFLCLPLFFSFHLYVALSAQPISTGVESV 325
Db 225 -----TIREKATVITLAAVVGAFVCFPFYFAVYRGGLGDDPVNEVEGCI 271
QY 326 VTWIGYFCFTSNPFYGGCLNROIQELSKOFVCFEKP--AADEELRL-----PSREG 375
Db 272 VLMIGYANSAINPLIYATLNDPRAVYQQLFCKLASHNSKRTSLRLNNSLSQSRREG 331
QY 376 SIENFLOLOGTGCPSSESVSRPLSPKQEP 407
Db 332 RMOEKKPLKQ-----VMSGTELTHPQSGP 356

RESULT 6
ALAD_RABIT STANDARD; PRT: 576 AA.
ID ALAD_RABIT STANDARD; PRT: 576 AA.
AC 002666;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALPHA-1D adrenergic receptor (Alpha 1D-adrenoceptor).
GN ADRAD.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97182161; PubMed=9030207;
RA Suzuki F., Miyamoto S., Takita M., Oshita M., Watanabe Y.,
RA Kakizuka A., Narumiya S., Taniguchi T., Muramatsu I.,
RT "Cloning, functional expression and tissue distribution of rabbit
RT alpha 1d-adrenoceptor."
RL Biochim. Biophys. Acta 1333:6-11(1997).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
CC THROUGH THE INFUX OF EXTRACELLULAR CALCIUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: U64032; AAB53098.1; -
DR GCRDB: GCR_1291; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 101
FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 102 126
FT DOMAIN 127 138
FT TRANSMEM 139 164
FT DOMAIN 165 174
FT TRANSMEM 175 197
FT DOMAIN 198 218
FT TRANSMEM 219 243
FT DOMAIN 244 256
FT TRANSMEM 257 280
FT DOMAIN 281 353
FT TRANSMEM 354 378
FT DOMAIN 379 385
FT TRANSMEM 386 410
FT DOMAIN 411 576
FT CARBOHYD 70 70
FT CARBOHYD 87 87
FT LIPID 424 424
FT DOMAIN 54 59
FT DOMAIN 78 84
FT DOMAIN 427 433
SO SEQUENCE 576 AA; 60266 MW; 21EDF1025D0144CE CRC64;

Query Match 14.9%; Score 345; DB 1; Length 576;
Best Local Similarity 25.0%; Pred. No. 8.6e-15;
Matches 128; Conservative 85; Mismatches 198; Indels 102; Gaps 19;

QY 4 SPIPOSSG--NSSTLGRPTGPSTASGVPEVGLRDVASSVAL-FMMLLDLTAAGN 60
Db 60 SVVGAGSGEDNRSSGEPGAGGGEVNGTAVGLVSAQSVGVLAAFTLTAAGN 119
QY 61 AAVNAVIAKTPALRKFFV--FVHLCVLDVLAATLPLAMSSALFPHALFGEVACRLY 118
Db 120 LVLIVSACNHNLOTVTFYVNLAVADLLSAIYLPSS--ATMEVGLFMAFGARFCQW 177
QY 119 LFLSVCFVSLAITSVAINVERYYVHPARYEVRMTGLVASVLYGVWVAKALMASVPV 178
Db 178 AAVDVLCTASILSLCTISVDVYGRHSLEKPAIMTERKAAATLALMLAVLVSMGPL 237
QY 179 LGRVSWERGASVPPGCSLQMSHSAVCOL-----FVVVFAVLYLLPLLLILVYCSMR 233
Db 238 LG---WKE---PVPP-----DERFCGITEVGAVFSSLSCFYLPMAVIVMVCRYV 284
QY 234 VAR--VAAHQGPLPTWMEPRORSES-----LSSRSTWVTSAGAPOT--TPHRTFEGG 283
Db 285 VARSTTNSLENG-----VRENGKASEVYVLRHCRKAASGADGAPETRGAKGHTFSS 337
QY 284 -----KAAVVLAVGQFLCLPLFFSFHLYVALSAQPISTGVESVVTWIGY 331
Db 338 LSVRLKFSREKKAAKTLAIYGVFLVCPFFVPLPGSLFPOLKPSGVFKYIFMLGY 397
QY 332 FCFTSNPFYGCCLNROIQELSKOFVCFK-----PAPEEEL 368
Db 398 FNSCVNPLIYCSSSEKFAFLRLRCQRRRRRRRPLRVYGHMWRASAGGHPDCL 457
QY 369 -----RLPREGSIEENFLQLOGTGCPSSESVSRP-----LSPKQEPAAV--DFRIPOQI 418
Db 458 SAGAAALPAA-----LALTAAPAPSSAAAPDEGAAGAGRRKPPCARERMLLGPL 507
QY 419 AETSEPLEDOLTDSDIIMSDSYLRPAASPRLES 451
Db 508 RRPIT-----QLRAKVSLSHKIRAGAGRAEA 535

RESULT 7
5H6_MOUSE STANDARD; PRT: 440 AA.
ID 5H6_MOUSE STANDARD; PRT: 440 AA.
AC 09R1C8;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Seroctonin receptor).
GN HTR6.
OS Mus musculus (Mouse).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Brain;
RA Kohen R., Guthe C.R., Heidmann D.E.A., Hamblin M.W.;
RL "Mutagenesis studies of the mouse 5-HT6 serotonin receptor.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS
CC A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC -----
DR EMBL: AF134158; AAD46490.1; -.
DR MCD: MGI:1196627; Hcr6.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 267 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 268 292 6 (POTENTIAL).
FT DOMAIN 293 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 322 7 (POTENTIAL).
FT DOMAIN 323 440 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 180 BY SIMILARITY.
FT CARBOHYD 9 9 N-LINKED (GLUCNA... (POTENTIAL).
SO SEQUENCE 440 AA; 46998 MW; 4440CDEBE01FEFC C66;
Query Match 14.88; Score 344; DB 1; Length 440;
Best Local Similarity 28.88; Pred. No. 7.8e-15;
Matches 134; Conservative 59; Mismatches 187; Indels 86; Gaps 19;

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OY 237 VAAMQHPLPYMTMETPROSESL-----SSRSTWYSSGAPOTPHRFGGKAAVLLAV 292
OY 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
DB 217 KQAVQVASLTGTGTATAGALETTLOVPRPRPGMSADSRRLTTHK-----SKKALKASFTL 272
OY 293 G---GQFLCMLPYFSEHLYVALSAQP-----ISTGQVESVWTWIGYRCFTSNPFYGLN 345
OY 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
DB 273 GILSMFVPTWLPFF-----VASIAQAVCDICISPLQFD-VLTWLGVCNSTWNPPIYPLFM 326
OY 346 ROIGELSKQVCFEKPAREE-----LRLP-----SREG 375
DB 327 RDEFRALGRFVPCVHC-PERHASPASPMWTSHSGARPGSLQOVLPLPSPNSDSA 385
OY 376 SIENFLOFLQTCGCPSESWSRPLSPKQBPAPVDFRIPQIAEE 421
DB 386 SGGTSGQLQTQQLLPGEA--TRDPPPTAPVYVNFVTSVEPE 429
-----
RESULT 8
HH2R_CAVPO STANDARD; PRT; 359 AA.
AC P47747;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histamine H2 receptor (H2R) (Gastric receptor 1).
GN HRH2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=Liver;
RA Traifort E.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
CC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC -----
DR EMBL: U25440; AAA65713.1; -.
DR GCRDB: GCR_1168; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 44 1 (POTENTIAL).
FT DOMAIN 45 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 81 2 (POTENTIAL).
FT DOMAIN 82 92 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 93 114 3 (POTENTIAL).
FT DOMAIN 115 134 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 135 159 4 (POTENTIAL).
FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 181 204 5 (POTENTIAL).
FT DOMAIN 205 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 258 6 (POTENTIAL).
FT DOMAIN 259 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 289 7 (POTENTIAL).
FT DOMAIN 290 359 CYTOPLASMIC (POTENTIAL).

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FT SITE 98 98 ESSENTIAL FOR HISTAMINE BINDING (BY
FT SITE 186 186 SIMILARITY).
FT SITE 186 186 ESSENTIAL FOR TIOTIDINE BINDING AND
FT SITE 186 186 IMPLICATED IN HISTAMINE BINDING (BY
FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING (BY
FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING (BY
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 91 174 BY SIMILARITY.
SQ SEQUENCE 359 AA: 40556 MW: 58DB81BD8FC30D9 CRC64:

Query Match 14.8%; Score 343; DB 1; Length 359;
Best Local Similarity 27.0%; Pred. No. 7.5e-15;
Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;

QY 49 MLILDLTAVAGNAAVAVIAKTPALRKRV--FVHLCVLVDLALTLPLALSSSLFD 106
DB 25 LILILVTVAGNAAVAVIAKTPALRKRV--FVHLCVLVDLALTLPLALSSSLFD 79
QY 107 HAL---FGEVACRLYLFLSVCFSVSLAISVAINVERYYVHPMYREVMRTGLVASVL 163
DB 80 LSCWSSSKFPCNITYTSLDWLCTASTLNLPMISLDRICAVTDPLRPVLTTPARVAISL 139
QY 164 VGVWAKALAAVAVLGRVSEGAAPVPPG---CSLQMSHAYCOLFVYVAVLYFL 218
DB 140 VEVIVISITISFLSI--HLGMSNRNEMSKNDITVCKQVQV---EYGLVDGIVTFY 192
QY 219 LPLILILVYCSMRVAVAAHOGPLTMEPTPORSSELSISSTVSTSGAQTTPHR 278
DB 193 LPLILIMITYFRIFKIRARINHHIGSMKAA----- 225
QY 279 TFGGKAAVVLAVAGGOFLLCMLFSPHLYVALSAQPISTGOVEVVTWIGFCFTSNP 338
DB 226 TIRHKATVTLAAWGFILICMFYFVYRGKGDANVEVEDVWLVGANSALNP 285
QY 339 FFYGCNLROJRGELSKOVCFKPAPEELRLP---SREGSIENFILOFGTCPSSESW 395
DB 286 ILVYALNRDFTAVAHQLECC-----RLASHNSHETSLRLNNSQ-LNRSCQCEPRW 334
QY 396 -VSRL 400
DB 335 QEDKPL 340

RESULT 9
HH2R_HUMAN STANDARD; PRT; 359 AA.
AC P25021; Q14464;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Histamine H2 receptor (H2R) (Gastric receptor 1).
GN HH2R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91337087; PubMed=1714721;
RA Gantz I., Munzert G., Tashiro T., Schaeffer M., Wang L.-D.,
RA DelValle J., Yamada T.;
RT "Molecular cloning of the human histamine H2 receptor.";
RL Biochem. Biophys. Res. Commun. 178:1386-1392(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=95275318; PubMed=7755641;
RA Nishi T., Koike T., Oka T., Maeda M., Futai M.;
RT "Identification of the promoter region of the human histamine H2-
RL receptor gene.";
RL Biochem. Biophys. Res. Commun. 210:616-623(1995).
RN [3]

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RP SEQUENCE FROM N.A.
RX MEDLINE=9297624; PubMed=10371214;
RA Murakami H., Sun-Wada G., Matsunoto M., Nishi T., Wada Y., Futai M.;
RT "Human histamine H2 receptor gene: multiple transcription initiation
RT and tissue-specific expressionl.";
RL FEBS Lett. 451:327-331(1999).
RN [4]
RP SEQUENCE OF 4-351 FROM N.A., AND POLYMORPHISM.
RC TISSUE=Brain;
RX MEDLINE=96414531; PubMed=8817552;
RA Orange P.R., Heath P.R., Wright S.R., Pearson R.C.A.;
RT "Allelic variations of the human histamine H2 receptor gene.";
RL Neuroreport 7:1293-1296(1996).
RN [5]
RP REVIEW.
RX MEDLINE=98042107; PubMed=9374694;
RA DelValle J., Gantz I.;
RT "Novel insights into histamine H2 receptor biology.";
RL Am. J. Physiol. 273:G987-G996(1997).
CC -I- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
CC ACID SECRETION. ALSO APPEARS TO REGULATE GASTROINTESTINAL MOTILITY
CC AND INTESTINAL SECRETION. POSSIBLE ROLE IN REGULATING CELL GROWTH
CC AND DIFFERENTIATION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY
CC G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND, THROUGH A SEPARATE
CC G PROTEIN-DEPENDENT MECHANISM, THE PHOSPHOINOSITIDE/PROTEIN KINASE
CC (PKC) SIGNALING PATHWAY (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- MISCELLANEOUS: ANTAGONISTS FOR THIS RECEPTOR HAVE PROVEN TO BE
CC EFFECTIVE THERAPY FOR ACID PEPTIC DISORDERS OF THE
CC GASTROINTESTINAL TRACT. CERTAIN ANTAGONISTS ARE USED IN THE
CC TREATMENT OF NEUROPSYCHIATRIC AND NEUROLOGICAL DISEASES SUCH AS
CC SCHIZOPHRENIA, ALZHEIMER'S DISEASE AND PARKINSON'S DISEASE.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M64799; AAA58647.1; -
DR EMBL; D49783; BA08618.1; -
DR EMBL; AB023486; BA084279.1; -
DR EMBL; X96133; CA66832.1; -.
DR PIR; JH0449; JH0449.
DR GCRDB; GCR_0176; -.
DR GCRDB; GCR_1836; -.
DR GCRDB; GCR_2080; -.
DR MTM; 142703; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRRHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 22
FT TRANSSEM 23 44
FT DOMAIN 45 57
FT TRANSSEM 58 81
FT DOMAIN 82 92
FT TRANSSEM 93 114
FT DOMAIN 115 134
FT TRANSSEM 135 159
FT DOMAIN 160 180
FT TRANSSEM 181 204
FT DOMAIN 205 234
FT TRANSSEM 235 258
FT DOMAIN 259 267
FT TRANSSEM 268 289
FT DOMAIN 290 359
FT SITE 98 98
ESSENTIAL FOR HISTAMINE BINDING (BY

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Db 4 EPCBV-----NSST---PAMGPPPPAPG-----GSGWAAALCVIIVLTA-AANS 45
QY 62 AVMAVIKTPALRK--VFVPHLCVLDLALTLMP LAMSSSLFPHALGGEVACRYL 119
Db 46 LLVILCTOPALRNTSNFVLSTSDLMGLVMPML--NALYGRWVLARGLCLMT 103
QY 120 FLVCFVSLATLSAIVNRYVYVHPMYREVRNTGLVSVLVGVVVKALAMASVPL 179
Db 104 AFDMWCSASLTNLCILSDRYLLILSLPKRLKNTAPRALALLGAMSLAALSLPL 163
QY 180 GRVSMEE-GAPSV-PGCSLOWSHSAYCOL-----FVVFAVLYFLPLLLLVYCSMF 232
Db 164 --LGMHELGKARTAPG-----QCRLASLPFVLAVAGVMEFLPSGALCFYCHIL 212
QY 233 RVAIVAMOHGRLPTWM-----ETPROSESSSSSTWVSSGAGQTPHRTFG 281
Db 213 LAARKQAVASLTGTGAGALETLQVPRTPRPMESADSRRLATKHSKAL----- 264
QY 282 GKAAVVLAVAGOLFCLMLPFYFSLYVALSAOPISFGVESVYTWIGFCTSNPEFY 341
Db 265 --KSLTLGLILGMFVYTWLPFVANAQAQV-CDCISGLFD-VLTWLGYNSTMNPIY 320
QY 342 GCLNRQIRGELSKQFCFKPAPEELRLP-----SREGSI 377
Db 321 PLFMRDEKRALGRPLPCVHCP-PENHPALPPPCGPIITAVPDQASACSRCLCICRQOI 379
QY 378 EENFLOFLOCT--GC---PSESWSRPLSPKQEP 407
Db 380 QTP---LQGAPRACSSQSPFCLELRPPGTPRHP 410

RESULT 11
B3AR_RAT STANDARD: PRT: 400 AA.
ID B3AR_RAT
AC P26255;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-3 adrenergic receptor.
GN ADRB3 OR ADRB3R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084710; PubMed=1721063;
RA Muzain P., Revelli J.-P., Kuhne F., Gocayne J.D., McCombie W.R.,
RA Venter J.C., Giacobino J.-P., Fraser C.M.;
RT "An adipose tissue-specific beta-adrenergic receptor. Molecular
RT cloning and down-regulation in obesity."
RL J. Biol. Chem. 266:24053-24058(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93178631; PubMed=8382630;
RA Bensaid M., Kachhad M., Rodriguez M., Je Fur G., Caput D.;
RT "The rat beta 3 adrenergic receptor gene contains an intron."
RL FEBS Lett. 318:223-226(1993).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
CC THERMOGENESIS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES, AND DIGESTIVE
CC TRACT.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).
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DR EMBL: M74716; AAA74470.1; -
DR EMBL: S73473; AAB20702.1; -
DR EMBL: S56481; AAB25520.1; -
DR EMBL: S56152; AAB25521.1; -
DR PIR: A41679; A41679
DR PIR: S29808; S29808.
DR PIR: A53281; A53281.
DR HSPB: P07700; IDEP.
DR GCRDB: GCR_0287; -
DR GCRDB: GCR_0622; -
DR GCRDB: GCR_0732; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 36
FT TRANSSEM 37 60
FT DOMAIN 61 69
FT TRANSSEM 70 88
FT DOMAIN 89 108
FT TRANSSEM 109 130
FT DOMAIN 131 152
FT TRANSSEM 153 175
FT DOMAIN 176 200
FT TRANSSEM 201 222
FT DOMAIN 223 289
FT TRANSSEM 290 311
FT DOMAIN 312 323
FT TRANSSEM 324 344
FT DOMAIN 345 400
FT CARBOHYD 8 26
FT DISULFID 107 186
FT LIPID 358 358
FT CONFLICT 234 235
SQ SEQUENCE 400 AA; 43146 MW; D588540C4B2CE813 CRC64;

Query Match 14.58; Score 337; DB 1; Length 400;
Best Local Similarity 28.28; Pred. No. 2e-14;
Matches 120; Conservative 65; Mismatches 188; Indels 52; Gaps 17;

QY 4 SPIPOSSGNSLTGRVPO-TPGPSTAGVPEVGRDVASEVALFMMLLDTLTVAGNAA 62
Db 2 APWHKNSLSLAFWSDAPITLDSANANTSGLPV-----PAAALAGALLALAVGGNLL 54
QY 63 VMAVIKTPALRK--VFVPHLCVLDLALTLMP LAMSSSLFPHALGGEVACRYL 120
Db 55 VITAIARTPRLQITITNVEVSLATADLVGLVMPG--ATIALTGHPILGATGCELTMS 112
QY 121 LSVCFVSLATLSAIVNRYVYVHPMYREVRNTGLVSVLVGVVVKALAMASVPL 180
Db 113 VDVLCVTRASITTCALADRYLATNPLRTGTLTKRRARAVALVWVSVATVSFAPLMS 172
QY 181 RVSMEEGAPSVPGCSLOWSHSAYCOL-----FVVFAVLYFLPLLLLVYCSMFRVA 235
Db 173 Q-WWRVAGDAAGQCH---SNPRCCSPASNNRYALLSSVSFYPLDLMFLVYARVFA 228
QY 236 ---RVAAMOHGRLPTWMETPR--QRSESLSSRTWVTSAGAP--TTPHR--TFGGCKA 285
Db 229 KRORRLRLRELGRPP--EESPRSPSRSPSPATVGTPTASDGVPCGRPARLPLGCHRA 287

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OY 286 AVLLANGGOLFCLWLPFSLHYVALSAQPISTGQVESVTVWIGYFCFTSNPFYGCIN 345
 DB 288 LRTGLIMGIFSLWLPFLANVRLATVGLSPGVFIANLWLGYSANSPNPLY-CRS 346
 OY 346 RQIGELSKOPVCFKPAPEBELR-----LPSREGSIDENFLOFLQNGCPSESIVS 397
 DB 347 PDFR-DAFRLLCSYGGGPEEPVYVTFPASVSRQNSPLNRF-----DGYEGE---- 395
 OY 398 RPLPS 402
 DB 396 RPPPT 400
 RESULT 12
 B3AR_BOVIN ID B3AR_BOVIN STANDARD: PRT: 405 AA.
 AC P46626: 028045: 09TSL17:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-3 adrenergic receptor.
 GN ADRB3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brown adipose tissue;
 RA MEDLINE=95324546; PubMed=7601122;
 RA Pletzl-Rouxel F., Lenzen G., Kapoor A., Drumare M.F., Archibault P.,
 RA Strosberg A.D., Manning B.S.J.;
 RT "Molecular cloning and pharmacological characterization of the bovine
 RT beta 3-adrenergic receptor";
 RT Eur. J. Biochem. 230:350-358(1995).
 RL 12
 RN SEQUENCE FROM N.A.
 RP STRAIN-Simmental;
 RC MEDLINE=20292453; PubMed=10834601;
 RA Forrest R.H., Hickford J.G.H.;
 RT "Rapid communication: nucleotide sequences of the bovine, caprine, and
 RT ovine beta3-adrenergic receptor genes";
 RT J. Anim. Sci. 78:1397-1398(2000).
 RL 13
 RP SEQUENCE OF 4-106 FROM N.A.
 RC TISSUE-Muscle;
 RA Scofield B., Meyer H.H.D.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RN 14
 RP SEQUENCE OF 156-298 FROM N.A.
 RC STRAIN-Friesian; TISSUE-adipose tissue;
 RA MEDLINE=94107293; PubMed=7904157;
 RA Castellana L., Wuzlin P., Revelli J.-P., Riequier D., Giacobino J.-P.;
 RT "Expression of beta 1- and beta 3-adrenergic-receptor messages and
 RT adenylylate cyclase beta-adrenergic response in bovine perirenal adipose
 RT tissue during its transformation from brown into white fat.";
 RL Biochem. J. 297:93-97(1994).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATCHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
 CC THERMOGENESIS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: X85961; CA59937.1; -.
 DR EMBL: AF109930; AAD26149.1; -.
 DR EMBL: X67214; CA47654.1; -.
 DR HSSP: P07700; IDEP.
 DR GCRdb: GCR_0627; -.
 DR GCRdb: GCR_1228; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1
 FT TRANSMEM 37 63
 FT DOMAIN 64 72
 FT TRANSMEM 73 91
 FT DOMAIN 92 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 178
 FT DOMAIN 179 203
 FT TRANSMEM 204 225
 FT DOMAIN 226 292
 FT TRANSMEM 293 314
 FT DOMAIN 315 326
 FT TRANSMEM 327 347
 FT DOMAIN 348 405
 FT CARBOHYD 8 8
 FT CARBOHYD 26 26
 FT DISULFID 110 189
 FT LIPID 161 361
 FT CONFLICT 6 7
 FT CONFLICT 156 156
 FT CONFLICT 156 156
 FT SEQUENCE 405 AA; 42903 MW; C93667DC1CC286f8 CRC64;
 Query Match 14.5%; Score 335.5; DB 1; Length 405;
 Best Local Similarity 28.1%; Pred. NO. 2,4e-14;
 Matches 121; Conservative 67; Mismatches 183; Indels 59; Gaps 18;
 OY 7 POSSGNSTLGRVQTP--GPST--ASGVPEVGLRDVASEVALFFMLLDITVAVGAA 62
 DB 3 PWPGRNSS-LTPWPDITPLAPNTNANSGLPVW---AVALLAGALLAVLATVGGNLL 57
 OY 63 VMVIAKTPALRKE--VFVHICLVDLIAALTLMPLAMISSALFDHALFEVACRLYLE 120
 DB 58 VIVAIARTPRRLQTMNVFVTSLATADLVGLVPPG--ATLALTGHMPPLGVTCGLMTS 115
 OY 121 LSCVPSIALISVAINVERYYVHPMYREVRMTGLIVASVLGVWVKALAMASVPLG 180
 DB 116 VDVLCTVPTASITETLCALAVDRYLAVTNPLRYGALVTKRRALAAVLLVWVSAVSFAFIMS 175
 OY 181 RVSMEDGAPSVPPCGSLQMSHSAVQGL-----FVVVFVAVLCELLPLLLIIVYCSMRVA 235
 DB 176 K-WRRIGDAQAQRCH--SNPRCCTFASNMPYVALLSSVSFYLLVLMLEVARVAVVA 231
 OY 236 ----RVAMQHGPPTMETPR--ORSELSRSTMYTSSGAP-----QTPPRTFGGG 283
 DB 232 TROLRLRLRELRGPRPESPAPRSRSGPLAGCASPAGPSYGRRRARLLPLREH--- 288
 OY 284 KAAVLLAVGQFLCLWLPFSLHYVALSAQPISTGQVESVTVWIGYFCFTSNPFYGC 343
 DB 289 RALRTGLIMGTFLCLWLPFSLHYVALSAQPISTGQVESVTVWIGYFCFTSNPFYGC 347
 OY 344 LNRQIGELSKOPVCFKPAPEBELR--PARESIDENFLOFLQNGCPSESIVS 401
 DB 348 RSPDFRSAR-RLLC--RCRPEHLAASPR-----APSGAPALTATSP 388
 OY 402 SPKOEPPAVD 411
 DB 389 AGPMQPEPLD 398

FT	DOMAIN	368	374		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	375	399		7 (POTENTIAL).
FT	DOMAIN	400	561		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	60	60		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	76	76		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	413	413		PALMITATE (POTENTIAL).
FT	DOMAIN	21	57		GLY-RICH.
FT	DOMAIN	416	421		POLY-ARG.
FT	CONFLICT	424	483		AVYCHHNRASITGDARDCAAPSPRIAPCAPLATLTAHHGAGS ADPEPTODVSSSRKPASA -> SLRPIALSDDRRAERLR POPSHRSPRGSSPHCTPGCGSLGNHADGAGCGLDOOSKASLR (IN REF. 1).
FT	SEQUENCE	561 AA;	59354 MM;	B6537/DCA44E7BE27 CRC64;	
SQ	Query Match	Best Local Similarity	14.5%;	Score 335.5;	DB 1; Length 561;
	Matches 125;	Conservative	25.7%;	Pred. No. 3.3e-14;	Mismatches 195; Indels 85; Gaps 19;
OY	6 IPQSGNSSTLGR-----VPQTGPSTASGVPEVGIRDVASEVAL-FPMLLLD	53	:	:	:
Db	42 VPGATGGGAAYVGTSGEDNQSTGEPCAAAGAEGVSAAYGLIYVSAQGVGVLPAFI	101	:	:	:
OY	54 LTAAGNAAMVAIVAKTPALKRFV--FVFHLCLVDLLAALLMPLAMLSSSLPFHALFG	111	:	:	:
Db	102 LTAAAGNLVLISVACNRRHQDTNTYTFVNLAADVADLLLSAAYLPPS--ATMEVLGFMAFG	159	:	:	:
OY	112 EVACRLYLELSCFVSIALILSVASAINVERYYVVHPREVEYMTGLVASVLYGVWKAL	171	:	:	:
Db	160 RTFCDDWAANDVLCCTASTLSLCTISVDRIYGVRRSLKYPALIMTKKAAILALLMAVAL	219	:	:	:
OY	172 AMASVPVLGRVSWEEGAPSVPGCSLOWSHSAYCOL----FVVFAVLYFLPLLILLY	226	:	:	:
Db	220 VVSQPLLG---WKE---PVPP-----DERFCGITEEVGYALFFSSVCSEFYLPMAVIYV	266	:	:	:
OY	227 VYCGMFRTAR--VAAMQHGPLTMMETPRKSE---SLSSSTMYTSSGAP--QTTPIRT	279	:	:	:
Db	267 MYCVVYVARSTRSTRLSEG---IKREP GKASEVLLRHCGAATSAAGYCPGTOSTSKGHT	322	:	:	:
OY	280 FGGG-----KAAVYLLAVGGQFLICMLPYEFSHLYVALSAOPISTNGVESVYT	327	:	:	:
Db	323 LRSSLRSRLKFESDEKKRAKTALIVGVYLCKMPFEFFVLPLGLSLFPDLKSEGVFKYIF	382	:	:	:
OY	328 WIGFYCFSTSNDFEYFGCLNQIRIGELSKQVCFKRPAREEELRLPSREGSIENFLQPILOG	387	:	:	:
Db	383 WLGFNFNCVNPDLIYPCSSRE-----FKRAFRLRLRCQR--RRRLMAVYG	427	:	:	:
OY	388 TGCSESSEWSNP--LPSPKOPRAYDPRI---PQIAIEETSEFLQLTSDLIIMSDSLRL	442	:	:	:
Db	428 HHMRASITGDARDCAAPSPRIAPCAPLATLTAHPGASADTPE-----TOPSVSSSR--K	479	:	:	:
OY	443 PAASPR 448		:	:	:
Db	480 PASALR 485		:	:	:
RESULT 14	B4AR MELGA	STANDARD:	PRT:	428 AA.	
ID	BAAR MELGA				
AC	PA3141;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	01-NOV-1995 (Rel. 32, Last annotation update)				
DE	Beta-4C adrenergic receptor.				
GN	ADBAC.				
OS	Meleagris gallinapavo (Common turkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauilia; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.				
NCBI	Taxid=9103;				
RN	[1]				
TX	SEQUENCE FROM N.A. MEDLINE=95014249; PubMed=7929160; Chen X.-H., Harden T.R., Nicholas R.A.: Molecular cloning and characterization of a novel beta-adrenergic				

```

RT receptor.
RL J. Biol. Chem. 269:24810-24819(1994).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS. MEDIANE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BROAD TISSUE DISTRIBUTION.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL: U13977; AAA62150.1; -.
CC EMBL: U13978; AAA62151.1; -.
CC HSSP: P07700; IDEP.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1.1; 1.
CC PRINTS: PR00237; GPCR_Rhodopsn.
CC PROSITE: PS00237; G-PROTEIN_RECPEP_F1_1; 1.
CC PROSITE: PS50262; G-PROTEIN_RECPEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 25
CC TRANSMM 26 49
CC DOMAIN 50 58
CC TRANSMM 59 77
CC DOMAIN 78 97
CC TRANSMM 98 119
CC DOMAIN 120 141
CC TRANSMM 142 164
CC DOMAIN 165 189
CC TRANSMM 190 211
CC DOMAIN 212 261
CC TRANSMM 262 283
CC DOMAIN 284 294
CC TRANSMM 295 315
CC DOMAIN 316 428
CC CARBOHD 8 8
CC CARBOHD 13 13
CC DISULFD 96 175
CC LIPID 329 329
CC SEQUENCE 428 AA: 47398 MW: 88203.20 DB3B8889 CXC64.

Query Match 14.5%: Score 335; DB 1; Length 428;
Best Local Similarity 27.3%: Pred. NO. 2.8e-14;
Matches 115; Conservative 59; Mismatches 179; Indels 68; Gaps 15;

OY 22 TTPSPATAGVPEVGLRDVASEVALFPHLLD-LRAVAGNAVMAVIATPLRKFF-VF 78
DB 2 TPLPAGNSVPCSWAAVLSRQMAVGAALSTILVIVAGNLLVIAVIAATPLQTMVNF 61
OY 79 VPHLCVLDLALTLPLMLAMSSALFDHALFGEVACRLTYLPLSCFVSLATLSAIV 138
DB 62 VTSLACADLVKMLLVVPR--ATILLSGHWPIGYVCELTSLDLVLCVATSIETLCATIV 119
OY 139 ERYVVVHPRMYEVMTGLVAVLVGVVWVAKALAMASVPLGRVSWEGAPSPGCCSIQ 198
DB 120 DRYLAITAPLYEALVTKGRAVAVVCMVAISAFISFLPMNH--MWRDQADBOAVRC-- 175
OY 199 MSHSAVQCL-----FVVVFAVLFLPLLLLVVYCSMRVA-----RVAAMQNG 243
DB 176 YDDPRCCFVTMTMTAIVASSTVSFVPLVLMFVVVRAVAVTRHVQLIGKDKVRLDEN 235
OY 244 PLPTMETPRORSESLSTWTSAGAPQTPPHRTFG--GGKAAVLLAVAGCOFLICWL 301
DB 236 P-----SLSSR-----GGWRRPSRLAIKEKALKLTGICITIGTTLICWL 275
OY 302 PYFSFHLVVALSAQPISTGVQSVVTVIGVFCFTSNPFYGLNQRINQELSKQFVCEFK 361

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DB 276 PEFVANL-IKVCRPLVPDQJLFLNMLGIVASARNPIIY-CRSPDFPSAFKLLCC--- 330
OY 362 PAPEELRLPSREGSIENFLQFLQGTGCPSESWSRPLPSKQPPAVDRIPQIAEE 421
DB 331 -----PRADRRLHAAPDPOHSC-----AFSPGDMEDESKAVD---PGLRED 373
OY 422 T 422
DB 374 S 374

RESULT 15
ALAD_HUMAN STANDARD: PRT: 572 AA.
ID ALAD_HUMAN
AC P25100.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
DE adrenergic receptor).
GN ADRA1D OR ADRA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RX MEDLINE=92028892; PubMed=1656955;
RA Bruno J.F., Whitaker J., Song J., Berelowitz M.;
RT "Molecular cloning and sequencing of a cDNA encoding a human alpha 1A
RL adrenergic receptor.";
RN Biochem. Biophys. Res. Commun. 179:1485-1490(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RX MEDLINE=94239386; PubMed=8183249;
RA Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,
RA Lepor H., Hartig P.R., Weinschenk R.L., Branchek T.A.,
RA Gluchowski C.;
RT "The alpha 1-adrenergic receptor that mediates smooth muscle
RT contraction in human prostate has the pharmacological properties of
RL the cloned human alpha 1C subtype.";
RN Mol. Pharmacol. 45:703-708(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwin D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA Wortman N.P., Campbell S., Fidock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues.";
RN J. Pharmacol. Exp. Ther. 272:134-142(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94296402; PubMed=8024574;
RA Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
RA Borowski D., Strader C.D., Bayne M.;
RT "Cloning, expression and characterization of human alpha adrenergic
RT receptors alpha 1a, alpha 1b and alpha 1c.";
RN Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Eshenshade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Mineman K.P., Murphy T.J.;
RT "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells.";
RL Mol. Pharmacol. 47:977-985(1995).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT

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QY 129 AIIVSATINVERYYYYVHHPMHEVEVRMLTGLVASTVGCWYKALMAASVPLVGRVSMIEGA 188
Db 183 SILSICTSYDVRYGVRRSLKTPAIMEKKAATLALMLVALVAVSGPLLG--WK- 237
QY 189 PSVPPGSGLSQMSHSAAYCOL-----FVVVFAVLYEPLPLLLLVVYCSMFYVAR--VMAQ 241
Db 238 -PVPP-----DERFGITEAGYAVFSSVCSFPLPMAVIVMYCRYVYVARSTTSLE 289
QY 242 HGPLTWMETPRKQSES-----LSSSTWVTSIGA--PQTHPTRTGGC----- 288
Db 290 AG-----VKREGKASSEVYLRIHCRGAATGAGAGAHOMRSAMKQHTFSSLSVRLKFSR 342
QY 284 --KAAYVLLAVGGQELLCMLPYFSFNLHYVALSAOPIHQGVESVYTWJIGYCFPTSNFFY 341
Db 343 EKKAAKTALVYGVFLVCLMFFFEFVYLVGLSFLPQLKPSGVCFKVIYFLMIGYNSCVNPLY 402
QY 342 GCLNRQIRGELSKEQVCFEK-----PAPEELRLPSREGSIEENPLQFL 389
Db 403 PCSSEFEKRAFLRLRLCCRRRRRRRRRLMYGHHMWRASTGLKODCAPSS----- 453
QY 386 OGTCQPSKSWMSRPLPSRKQEPRAV-----DFRLPGQALETSEPLE 427
Db 454 -GDAPPGAVPLTLVLPDDPEPPCTPEKQAPVASRRKPPSAFEMERLGLGPPRRPT---- 506
QY 428 QQLTSDIIMSDSYLRPAASPRLES 451
Db 509 -QLRAKVYSLSHKIRAGAGQARA 531

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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:11 : Search time 33 Seconds
(without alignments)
2364.264 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318
Sequence: 1 MESSPIPOSSGNSSTLGRVP.....SDIIMSDYLRLPAPSRLES 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP virus:*
- 16: SP bacteriaph:*
- 17: SP archaep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2308	99.6	451	4	Q96PR4
2	2106	90.9	417	4	Q9BZJ8
3	438.5	18.9	358	11	Q9BZJ7
4	347	15.0	358	11	Q9OX37
5	347	15.0	397	11	Q9D282
6	333.5	14.4	571	6	Q9TMM9
7	330.5	14.3	405	6	Q9GJS6
8	329	14.2	407	6	Q9MZ00
9	328	14.2	438	11	Q63004
10	327.5	14.1	405	6	Q9GJ70
11	327.5	14.1	405	6	Q9GL56
12	326.5	14.1	405	6	Q9GL57
13	322	13.9	399	5	Q9NG02
14	318.5	13.7	402	13	Q9OX46
15	316.5	13.7	559	11	Q9QW71
16	306	13.2	466	4	Q96RE8

17	304	13.1	515	11	Q9DBL0	Q9db10 mus musculus
18	302.5	13.0	464	5	Q9GQ54	Q9gq54 aedes aegypti
19	301	13.0	518	6	Q9MY18	Q9my18 oryctolagus
20	300	12.9	429	4	Q13729	Q13729 homo sapien
21	300	12.9	455	4	Q60451	Q60451 homo sapien
22	300	12.9	499	4	Q13675	Q13675 homo sapien
23	299.5	12.9	378	4	Q96KH9	Q96kh9 homo sapien
24	299	12.9	429	6	Q9MKU3	Q9mku3 oryctolagus
25	297	12.8	466	4	Q9UD63	Q9ud63 homo sapien
26	296	12.8	466	6	Q9MZ02	Q9mz02 oryctolagus
27	292.5	12.6	603	5	Q9VG57	Q9vg57 drosophila
28	291.5	12.6	387	4	Q96K10	Q96k10 homo sapien
29	288.5	12.4	419	5	Q77254	Q77254 boophilus m
30	287	12.4	466	6	Q9TSM7	Q9tsm7 sus scrofa
31	284.5	12.3	385	5	Q24038	Q24038 drosophila
32	283	12.2	407	4	Q75963	Q75963 homo sapien
33	282	12.2	445	13	Q98841	Q98841 anguilla an
34	281.5	12.1	407	5	Q9VGS4	Q9vg54 drosophila
35	281	12.1	466	11	Q54913	Q54913 cyprinus ca
36	280.5	12.1	437	13	Q42316	Q42316 cyprinus ca
37	279.5	12.1	466	13	Q42315	Q42315 cyprinus ca
38	279	12.0	402	5	Q44198	Q44198 apis mellif
39	278.5	12.0	422	6	Q9N296	Q9n296 pongo pygma
40	278.5	12.0	508	5	Q9VC23	Q9vc23 drosophila
41	277.5	12.0	349	4	Q9UD67	Q9ud67 homo sapien
42	277.5	12.0	422	6	Q9N297	Q9n297 gorilla gor
43	276.5	11.9	422	6	Q9N298	Q9n298 pan troglod
44	276.5	11.9	445	13	Q98842	Q98842 anguilla an
45	274.5	11.8	470	11	P97842	P97842 rattus norv

ALIGNMENTS

RESULT 1
ID Q96PR4 PRELIMINARY; PRT: 451 AA.
AC Q96PR4:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE BIOGENIC AMINE RECEPTOR-LIKE PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cikos S., Gregor P., Koppel J.;
RT "Cloning of a novel biogenic amine receptor-like G protein-coupled
RT receptor expressed in human brain.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258342; AAK97826.1; -
KW Receptor.
SQ SEQUENCE 451 AA; 49308 MW; 4CAA22D1E7B8882 CRC64;

Query Match	99.6%	Score 2308	DB 4	Length 451
Best Local Similarity	99.6%	Pred. No. 6.5e-194		
Matches 449	Conservative 1	Mismatches 1	Indels 0	Gaps 0
QY 1	MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEGLDVASESVALPFMLLDLTAAGN 60			
Db 1	MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEGLDVASESVALPFMLLDLTAAGN 60			
QY 61	AAVAVIAKTPALRKFFVFFHLCVLDLAAATLPLAMLSALFDHALGFEVACRLYL 120			
Db 61	AAVAVIAKTPALRKFFVFFHLCVLDLAAATLPLAMLSALFDHALGFEVACRLYL 120			
QY 121	LSVCFVSLATLSVAIVERYYYVHPMRVREKRTLDLVASVYGVVAKLAASVPLG 180			
Db 121	LSVCFVSLATLSVAIVERYYYVHPMRVREKRTLDLVASVYGVVAKLAASVPLG 180			
QY 181	RVSMEGAPSVPCPSLQWMSHAYCOLFVVVFAVLFLPLLLTLVYCSMFRVAVAA 240			

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|||||
Db 181 RVSEBAPSVPCSLQWHSAYCOLFVVVFAVLYELLPLLLLVYCSMFRAVAAM 240
Qy 241 OHGLPTWMEPRORSLSRSRTMTSSGAPOTPHRTGGGAAVYLLAVGGQFLCW 300
Db 241 OHGLPTWMEPRORSLSRSRTMTSSGAPOTPHRTGGGAAVYLLAVGGQFLCW 300
Qy 301 LPVFSFLVYALSAQPISTGVESVWTWIGFCTSNPFYGCINROI RGLSKQVCF 360
Db 301 LPVFSFLVYALSAQPISTGVESVWTWIGFCTSNPFYGCINROI RGLSKQVCF 360
Qy 361 KPAEBELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Db 361 KPAEBELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Qy 421 ETSEFLQOLTSDIIMSDSYRPAASPRLES 451
Db 421 ETSEFLQOLTSDIIMSDSYRPAASPRLES 451
```

RESULT 2

```
09BzJ8 ID 09BzJ8 PRELIMINARY: PRT: 417 AA.
AC 09BzJ8:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN GPR61.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105913; Pubmed=11165367;
RA Lee D.K., Cheng R., Nguyen T., Liu Y., Brown M., Lynch K.R.,
RA George S.R., O'Dowd B.F.;
RT "Identification of four novel human G protein-coupled receptors
RT expressed in the brain."
RL Brain Res. Mol. Brain Res. 86:13-22(2001).
DR EMBL: AF317652; AAK12637.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SQ SEQUENCE 417 AA; 45606 MW; 3475BD4F1A714FF2 CRC64;
```

Query Match 90.9%; Score 2106; DB 4; Length 417;

Best Local Similarity 98.8%; Pred. No. 2.9e-176; Matches 409; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASEVALFEMLLDLTAAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASEVALFEMLLDLTAAGN 60
Qy 61 AAVAVAIAKTPALKKFFVFLCLVDLLAATLTPMLAMSSALFDHALPGEVACRLYL 120
Db 61 AAVAVAIAKTPALKKFFVFLCLVDLLAATLTPMLAMSSALFDHALPGEVACRLYL 120
Qy 121 LSVCFVSLAITSVAIINVERYYVHPMRREVRMTGLVAVLVGVVWKALAMASVPLG 180
Db 121 LSVCFVSLAITSVAIINVERYYVHPMRREVRMTGLVAVLVGVVWKALAMASVPLG 180
Qy 181 RVSEBAPSVPCSLQWHSAYCOLFVVVFAVLYELLPLLLLVYCSMFRAVAAM 240
Db 181 RVSEBAPSVPCSLQWHSAYCOLFVVVFAVLYELLPLLLLVYCSMFRAVAAM 240
Qy 241 OHGLPTWMEPRORSLSRSRTMTSSGAPOTPHRTGGGAAVYLLAVGGQFLCW 300
Db 241 OHGLPTWMEPRORSLSRSRTMTSSGAPOTPHRTGGGAAVYLLAVGGQFLCW 300
Qy 301 LPVFSFLVYALSAQPISTGVESVWTWIGFCTSNPFYGCINROI RGLSKQVCF 360
Db 301 LPVFSFLVYALSAQPISTGVESVWTWIGFCTSNPFYGCINROI RGLSKQVCF 360
Qy 361 KPAEBELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Db 361 KPAEBELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Qy 421 ETSEFLQOLTSDIIMSDSYRPAASPRLES 451
Db 421 ETSEFLQOLTSDIIMSDSYRPAASPRLES 451
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|||||
Qy 301 LPVFSFLVYALSAQPISTGVESVWTWIGFCTSNPFYGCINROI RGLSKQVCF 360
Db 301 LPVFSFLVYALSAQPISTGVESVWTWIGFCTSNPFYGCINROI RGLSKQVCF 360
Qy 361 KPAEBELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Db 361 KPAEBELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
```

RESULT 3

```
09BzJ7 ID 09BzJ7 PRELIMINARY: PRT: 368 AA.
AC 09BzJ7:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN GPR62.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105913; Pubmed=11165367;
RA Lee D.K., Cheng R., Nguyen T., Liu Y., Brown M., Lynch K.R.,
RA George S.R., O'Dowd B.F.;
RT "Identification of four novel human G protein-coupled receptors
RT expressed in the brain."
RL Brain Res. Mol. Brain Res. 86:13-22(2001).
DR EMBL: AF317653; AAK12638.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SQ SEQUENCE 368 AA; 37628 MW; 9CFF95298D12C75 CRC64;
```

Query Match 18.9%; Score 438.5; DB 4; Length 368;

Best Local Similarity 31.8%; Pred. No. 2.5e-30; Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

```
Qy 40 ASE---SVAFEMLLDLTAAGNAVAIAKTPALKKFFVFLCLVDLLAATLTPML 96
Db 9 ASEVAGSLGLLAIVAEVGLGALLVYLRPRGLRDLALYHLCLVDLLAASIMPL 68
Qy 97 AMSSSAL-FDHALPGEVACRLYLFSVCFVSLAITSVAIINVERYYVHPMRREVRMT 155
Db 69 GLLAAPPGLGRVRLGPAARFELSAAALIPACTLGVAALGLARYRLIVHPRGSRPP 128
Qy 156 LGIVASVLGVVWVWALAMASVPLGVRVSEBAPSVPCSLQWHSAYCOL-----F 208
Db 129 PVL---VLTAVMAAAGLGLSL-----GPPAPPPA-----PARCSVLAGGLGPF 172
Qy 209 VVFAVLYELLPLLLLVYCSMFRAVAAMQHPLPTWMEPRORSLSRSRTMTSS 268
Db 173 RPLWALLAFALPALLLLGAVGIFVVARAALR-PPRPA--RGSRLSDSLDRLSTL- 227
Qy 269 SGAPOTPHRTGGGAAVYLLAVGGQFLCWLPIFSFHLVYALSAQPISTGVESVWT 328
Db 228 ---PPLRPR-LPGCKAALPALAVGOFACWLPY-----GCACLAARAAEAETV 277
Qy 329 IGVCFCTSNPFYGCINROI---GELSKQVCFKPAEBELRLPSREGSIEENFLQ 385
Db 278 VAASAFAPHPFLGLDPRVKALGLRSLRRL-----GPPVR----- 314
Qy 386 QGTGCPSESWSRPLPSKQEPVADFRIPQIAEETSE 424
Db 315 ---ACTPQAHPRALDLOCLOPRPGPAVGPSEARPDQIRE 350
```

RESULT 4

090x37
ID 090x37 PRELIMINARY: PRT: 358 AA.
AC 090x37
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HISTAMINE H2 RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ;
RA Fukushima Y., Asano T., Sugano K.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF019138; AAD01634.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1; GPCR_Rhodpsn.
DR PRINTS: PR00237; GPCR_Rhodpsn.
DR PROSITE: PS00237; G-PROTEIN_RECPEP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40284 MW; D270C2C66AB7A256 CRC64;

Query Match 15.0%; Score 347; DB 11; Length 358;
Best Local Similarity 27.6%; Pred. No. 2.5e-22;
Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;

QY 42 ESVALFEMLLDLT-----AVAGNAAVAVIAKTPALRKFV--FVHLCVLDLLAALTL 94
DB 13 DSIALKVTISVLTLTITITVAGNVVCLAVSLNRLSLNCFIVSLAATDILGLLVM 72
QY 95 PLAMSSALFDHAL---FGEVACRLYLFLSYCFVSLAILSYAINVERYYVHPMYE 151
DB 73 PF-----SAIQLSFKMSFGVFCNIYTSLDVMTCTASILNFMISLDRYCAVDPLEKYP 127
QY 152 VRMTIGLVAASLVGVWAKALMAASVPVIGRVSWEE-----GAPSVPPGCSLONSHSAYC 205
DB 128 VLVTPVRAISLVFIWISITLSFLSI--HLGWSNRNGTRGNDTFK--CKQVNV----- 178
QY 206 QLEVVFAVLYFLPLLLILVYVCSMFVARVAAMQHPLPTMPTPRQSRSSLSRSTM 265
DB 179 EYGLGDGMVTFYLPILIMCTYTRIFKIRAOAKRINHISWKAA----- 224
QY 266 VTSSGAPOTTTHRTFGGKAAVLLAVGQFLCMLPYFSFHLVYALSAPISTGVESV 325
DB 225 -----TIREHKAATVTLAAVMGAFIVCMFPYFTAFVYVGLGDDAVNEVGEI 271
QY 326 VTWIGYFCFTSNPFYVGLNROIRGELSKOYVCFEKP--APEEELRL-----PSREG 375
DB 272 VLMIGYANSALNPILYATLNDFRMAVYQDLPHCKLASHNSHKTSILRLNNSLSRSQSRG 331
QY 376 SIENFLOFLOGTGCPSESWSRPLPSKQEP 407
DB 332 RMQEEKPLKQ-----VMSGTELTTHPQSGP 356

RESULT 5
09D282 PRELIMINARY: PRT: 397 AA.
AC 09D282
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HISTAMINE RECEPTOR H 2.
GN HRH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CECUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barb G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita S., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AK020259; BAB3204.1;
DR MGD: MGI:108482; Hrh2.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1; GPCR_Rhodpsn.
DR PRINTS: PR00237; GPCR_Rhodpsn.
DR PROSITE: PS00237; G-PROTEIN_RECPEP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 397 AA; 44793 MW; BB4719084F4BDD5 CRC64;

Query Match 15.0%; Score 347; DB 11; Length 397;
Best Local Similarity 27.6%; Pred. No. 2.8e-22;
Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;

QY 42 ESVALFEMLLDLT-----AVAGNAAVAVIAKTPALRKFV--FVHLCVLDLLAALTL 94
DB 13 DSIALKVTISVLTLTITITVAGNVVCLAVSLNRLSLNCFIVSLAATDILGLLVM 72
QY 95 PLAMSSALFDHAL---FGEVACRLYLFLSYCFVSLAILSYAINVERYYVHPMYE 151
DB 73 PF-----SAIQLSFKMSFGVFCNIYTSLDVMTCTASILNFMISLDRYCAVDPLEKYP 127
QY 152 VRMTIGLVAASLVGVWAKALMAASVPVIGRVSWEE-----GAPSVPPGCSLONSHSAYC 205
DB 128 VLVTPVRAISLVFIWISITLSFLSI--HLGWSNRNGTRGNDTFK--CKQVNV----- 178
QY 206 QLEVVFAVLYFLPLLLILVYVCSMFVARVAAMQHPLPTMPTPRQSRSSLSRSTM 265
DB 179 EYGLGDGMVTFYLPILIMCTYTRIFKIRAOAKRINHISWKAA----- 224
QY 266 VTSSGAPOTTTHRTFGGKAAVLLAVGQFLCMLPYFSFHLVYALSAPISTGVESV 325
DB 225 -----TIREHKAATVTLAAVMGAFIVCMFPYFTAFVYVGLGDDAVNEVGEI 271
QY 326 VTWIGYFCFTSNPFYVGLNROIRGELSKOYVCFEKP--APEEELRL-----PSREG 375
DB 272 VLMIGYANSALNPILYATLNDFRMAVYQDLPHCKLASHNSHKTSILRLNNSLSRSQSRG 331
QY 376 SIENFLOFLOGTGCPSESWSRPLPSKQEP 407
DB 332 RMQEEKPLKQ-----VMSGTELTTHPQSGP 356

RESULT 6
09TTM9 PRELIMINARY: PRT: 571 AA.
AC 09TTM9

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALPHA-1D ADRENERGIC RECEPTOR.
GN ALPHA-1D.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Uhlen S., Wralth A.;
RT "Characterization of the pig alpha-1D adrenergic receptor."
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ250492; CAB59347.1; -
DR EMBL: AJ250493; CAB59347.1; JOINED.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
KM G-protein coupled receptor; Glycophorin; Receptor; Transmembrane.
SO SEQUENCE 571 AA; 60698 MW; BACFE35C903972B1 CRC64;

Query Match	14.48	Score 333.5	DB 6	Length 571
Best Local Similarity	24.08	Pred. No. 6.3e+21		
Matches 125	Conservative 85	Mismatches 201	Indels 109	Gaps 17

QY	6	IPQSGVSNSTIGRPO-----TPPST-----SCVPEGLADVSEVAL-FEFLLL	52
Db	46	VPGTAGSGGVGCASDENNRNSACEPCAGAGGEVNTAAVGGIYVSAQGVGVFLAA	105
QY	53	DLTVAGNAAVMAVIATKPRV--FVHLLVDLLAALTPLMLMSLLFDHALF	110
Db	106	ILMAVAGNLLVLEISVACNRHLQDTNTNFIVNLAADLLSATVLPFS--ATMEVLGFMAF	163
QY	111	GEVACRLVLFVSGFSLATVSAINVERYYVVMRYREVRMTGLVASVVGWVKA	170
Db	164	GRACDVMADVLCCTASILSLCTISVDRIYGVRIHSLKPISTETEKAAAILALMVA	223
QY	171	LAMASVPLGVHSNEGAPVPPGCSLQWSHSAYQCL----FVYFAVLVFLPLLLIL	225
Db	224	IVVSGVPLLG--MKE--PVPP-----DERCCGTEAGYAVFSSLCFLPMIAIV	270
QY	226	VVYSGMEFVARVAMQNPPLPTMEPRPQSESLSSKSTWVTS-----GAPQTPHR	278
Db	271	VMYCRVYVVARSTRS---LEAGYKREGRKASEVYLAIHCRGSSGTGDRHGAMRSTKG	327
QY	279	TFGGG-----KAAVYLLAVGQFLLCWLPHYSEHLVVALSAQDISTGOEVS	326
Db	328	TFRSSLSLRLLFSREKKAATKTLIVGVLELCMFPEFFVLPLGSLPPQLKPSGEVKI	387
QY	327	TWIGYFCTSNPFYGGCINRIQBELSKQVCFPK-----PA	363
Db	388	FWLGTENSCVNPPLIYPCSSREFKAFRLRLRCQCHSRRRRRRLMRYAGHHMLASNGPR	447
QY	364	P-----EELRLPSREGSIENFLQFLQTCGPSESWSRPLSPKQEPRAV-D	411
Db	448	PDCAPGLGAAPREAPLAPAE-----ATDTPSAPEAQAVVGRKRPYSFRD	455
QY	412	FRIGQIALEETSEFLBOOLTSDIIMDSYLPRAPSPLES	451
Db	496	WRLLGPPRRPTT-----QLRKVVSSLSQKIRAGAPCAEA	530

RESULT 7	
09GJS6	
ID 09GJS6	PRELIMINARY;
AC 09GJS6;	PRT; 405 AA.
DT 01-MAR-2001	(TREMBLrel. 16, Created)
	(TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE BETA 3 ADRENERGIC RECEPTOR.
GN B3AR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Hordidae; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
NCBI_TaxID=9940; Ovis.
OX

RP SEQUENCE FROM N.A.
RA Forrest R.H., Hickford J.G.H.;
RT "Polymorphism within the ovine beta 3 adrenergic receptor gene.";

CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
DR EMBL; AF314204; AAC31167.1; -.

```
DR InterPro; IPR000276; GPCR_Rhodpsn.  
DR Pfam; PF00001; 7tm_1; 1.  
DR PRINTS; PR00237; GPCR_RHODOPS_N.
```

DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 405 AA; 42928 MW; A0DD3AEBAF814E75 CRC64;

Query Match	14.3%	Score 330.5;	DB 6;	Length 405;
Best Local Similarity	29.4%;	Pred. No. 7.9e-21;		
Matches 116; Conservative	62;	Mismatches 170;	Indels 47;	Gaps 10;

QY 7 PSSGNSSTLGRVPTP--GPSF--ASGVPEGLRDVAASESVAFEMLLDITAVAGNNA
+ + + + + | : : + + + + +
Db 3 PMPGNS-LTPWPIPTLPANTANASGLGPW----AVALAGLLALAVATVGNNL

QY 63 VMAVIAKTPALRKF--VEVFHCLVDLIALTLMLPLAMISSALEFDHALFGEVACRLYLE
+ : + : + : + : + : + : + : + : + : + : + : + : + : + : + : + :
Db 58 VVAIARPPRLQMTNVFVTSLATADLVGLLVPPG--ATLALTGHMPLGVTCCELWTS

QY 121 LSCVFSIALILSVAINVERYYVVHPMKREVRMTGLVASVLGVWKALAMASVPVLG
 : | : : : : : | : : : : :
Db 116 VDLVCVASIETICLAVDRYAATNPLRGALVTKRRAAAVYLWVWSAASVFAPIPS

QY 181 RVSMEGAPSVPPGCSLQWMSHAYCQL-----FVVVFVAVLFLPLLLILVYCSMFRA
: | || : | : : : : | |||| : | ||
Db 176 K-WNRVSGDAEAQRH---SNRQCTFASNPYALISSVSFYPLVLMFLYARVFAVA

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QY      236  ----RVAMQHGPLTWMETPR-QRSESLSSKSTVMVSSGAP-----QTTPHRTFGGG
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      232  TRQLRLRLRELGREPEESPAPASRSGSPGAPGAPYASAPAGVPSYGRPPARLLPLREH---

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Oy 284 KAANVLLAVGGQFLCWLPIESFHLVVAISAQPISTGOVESVTWIGYFCFTSNPFYGC
:
Db 289 RALRTIGLIMGTFFLCWLPIEFVVNVVRALGGPSLVSPTEIALMWIGYASAEPLIYC

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OY      344 LNRQIRGELSKQFVCFKPAPEEEL-----RLPS 372
        : | : : : |
Db      348 RSPDFRSAF-RRITC--RCPPREHTAAASPAPAS 379

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RESULT 8
000700

ID	Q9MZ00	PRELIMINARY;	PRT;	407 AA.
AC	Q9MZ00;			
DT	01-OCT-2000	(TReMBLrel, 15, Created)		
DT	01-OCT-2000	(TReMBLrel, 15, Last software update)		

DT 01-DEC-2001 (Tremblé et al., 19, last annotation update)
DE BETA-3-ADRENERGIC RECEPTOR.
OS Sus scrofa (Pig).

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

RA Smith T.R., Bidwell C.A., Mills S.E.;

Query Match	14.3%;	Score 330.5;	DB 6;	Length 405;
Best Local Similarity	29.4%;	Pred. No. 7.9e-21;		
Matches 116;	Conservative 62;	Mismatches 170;	Indels 47;	Gaps 17

7 POSSGSSSTLGRVPQT--GPST--ASGVPEVGLRDVASESVALFFMLLLDITAVAGNNA 62
+ ||||| - - - - - : : | ||| : - - - - - : : | |||
3 PMPGSSS-LTFPMDIPTLAPNTANASGLPGPW----AVLAGALIALAVLATVGGNLL 57

63 VMVAVIKTPALRKF--VEVFHLCVLDDLAAITLMPFLAMLSSALFDHALFGEVACRLYLEF 120
+ : ||::|| : ||| | : || : : || :
58 VIVAIARTPILOTMTNFEVTSLATADLVGLLVPPG-ATLALNGHPILGVTCCELMTS 115

[illegible]

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181 RVSMEGAPSVPPGCSLQMSHAYCQ-----FVVVFAVLFLPLPLILLVYCSMFVA 235
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
176 K-WMRVGADEAQRCH-----SNPQCTFASNMPLYALLSSVFFYLPLVMLFVYARVFEVA 231
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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236 ----RAAAMQHGPLPTWMETPR-QRSELSLSRSTWVTSSGAP-----QTTPHRTFCGG 283
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
232 TROLRLRLRRLGRRPEESPAPSRSGSPGAPAPASAPAGPSYGRRRPRLPLRFH---- 288

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[illegible]

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344 LNRQIGELSKQVCFKPKAPEEEL-----RLPS 372
      : | :: : ||| |
348 RSPDFRSAP-RRILIC--RCPDEFHIAASDPBAPS 379

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RESULT 8
19M700

D	Q9M200	PRELIMINARY;	PRT;	407 AA.
C	Q9M200;			
T	01-OCT-2000 (TREMBLrel. 15, Created)			
T	01-OCT-2000 (TREMBLrel. 15, Created)			

01-DEC-2001 (Tremblay et al., 1999, last annotation update)
BETA-3-ADRENERGIC RECEPTOR.
Sus scrofa (pig).
Submitted by: V. L. ...

C Mammalia; Euthera; Cetartiodactyla; Sulna; Suidae; Sus.
X NCBI_TaxID=9823;
N [1]

A. Smith T.R., Bidwell C.A., Mills S.E.;

RT "Sus scrofa beta-3-adrenergic receptor (BAR3) gene."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL: AF274007; AAF82301.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 407 AA; 43610 MW; C6598382A9B38DD9 CRC64;

Query Match 14.2%; Score 329; DB 6; Length 407;
 Best Local Similarity 28.6%; Pred. No. 1.1e-20;
 Matches 125; Conservative 61; Mismatches 177; Indels 74; Gaps 21;

OY 4 SPIPOSSGNSSTIGRVPOTPGPST-----ASGVEVGLRDVASEVALPFMLLD-L 54
 DB 2 APWPQ--GNSS-----LPPRPDYSTLAPNMANSGLRGV-----PMAVALAGALLAPVL 49
 OY 55 TAVGNAAMAVIAKTPALRKF--VFPHLCVLDLLALTLPLMLSSALFDHALFGE 112
 DB 50 AVVGNLLVIAIARTPLQWTNVEVTSIATADLVGLVLPVPG--TTIALTGHMPLGA 107
 OY 113 VACRLYLEVSGFSLATLSVAINVERYYVHPREYVMTGLVASLVGVVKKALA 172
 DB 108 TCCELMTSVDVLCYASLETLCALAVDRILAVTNPKRGALTKRRARAVALVWVNSA 167
 OY 173 MASVEVLGRVSEGAAPVPCSLQWSSHAYCOL-----FVVVFAVLVFLPLLLIV 227
 DB 168 VSFARIMSK--MWRVGADADAQRCH---SNPSCCTFASNPVYLLSSVSFYLLVLMLEF 223
 OY 228 YCSMRVARVAMOGRLPTW--METPKROSESLSRSTMTSSGAPOTTPHRTGGGKA 285
 DB 224 YARVF-----VATSQLRLRLMELSRFPPEESPAPSRK--QSPAPGRPMSPAGVPSHGRR 278
 OY 286 AVLL-----AVGQFLLCMLPYFSFHLVYALASAPISITGQVESVVTMIGYC 333
 DB 279 PARLLPLREHRACTLGLIMGTFTLCMLPFYVNVNRRALGSPSLVPAPFALMLNGAN 338
 OY 334 FTSNPFYGLNROIRGELSKQVCFKPAPEELRL--PSREGSIENFLOFLOGTGCP 391
 DB 339 SAFNPLIY-CHSPDRSAF--RRLLC--RCGPPEHLAASPPAPR-----GAP 382
 OY 392 SESWVSRLPSKQEP 408
 DB 383 ET--LTHPAES--RQSP 396

RESULT 9
 O63004 PRELIMINARY; PRT; 438 AA.
 ID O63004;
 AC O63004;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 5-HT6 SEROTONIN RECEPTOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=STRATUM;
 RA MEDLINE=96102917; PubMed=8522988;
 RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
 RA Meltzer H.Y., Sibley D.R., Roth B.L., Hamblin M.W.;
 RT "Cloning, characterization, and chromosomal localization of a human 5-
 RT HT6 serotonin receptor."
 RL J. Neurochem. 66:47-56(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL: L41146; AAN92633.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 438 AA; 46786 MW; DB90403892F691A9 CRC64;

Query Match 14.2%; Score 328; DB 11; Length 438;
 Best Local Similarity 27.4%; Pred. No. 1.4e-20;
 Matches 129; Conservative 61; Mismatches 184; Indels 96; Gaps 19;

OY 2 ESSPIPOSSGNSSTIGRVPOTPGPSTASGVPEVGLRDVASEVALPFMLLDLTVAAGNA 61
 DB 4 EPGPV-----NST--PAMGPGPPAPG-----GSGVMAALCVIYVLTG-AANS 45
 OY 62 AMAVIAKTPALRKF--VFPHLCVLDLLALTLPLMLSSALFDHALFGEVACRLYL 119
 DB 46 LLIVLICQPAVRNTSNFFVLSFTSDLMVGLVMPAPML--NALYGRVILARGICLLMT 103
 OY 120 FLVSGFSLATLSVAINVERYYVHPREYVMTGLVASLVGVVKKALAMASVPL 179
 DB 104 AFDVMCCSASITLNCILSIDRLLIISPLRYKLRMTAPRALALIGAMSLAASFLPL 163
 OY 180 GRVSNME--GAPSV--PCGSLQWSSHAYCOL-----FVVVFAVLVFLPLLLVYCSMF 232
 DB 164 --LGWHEIKARTPAPG-----OQRLASLPFLVASGVTFELBSGALCFYTCRL 212
 OY 233 RVARVAMOGRLPTWMM-----ETPKROSESLSRSTMTSSGAPOTTPHRTFG 281
 DB 213 LAARKQAVQVASTLTGTAGQALETLQVPTPRPGMESADSRRLAKHNSKAL----- 264
 OY 282 GKAAVVLVANGGQRLCMLPYFSFHLVYALASAPISITGQVESVVTMIGYFCFTSNPFY 341
 DB 265 --KASLTGLIGLMFVFVWLPFFVANIAQAV--CDICISPLFD-VLTWLYGCNSTMNPITY 320
 OY 342 GCLNQIRGELSKQVCFKPAPEE-----LRLP----- 371
 DB 321 PLFMDFKKALGRPLPCVHCP--PEHRASPAASPMKTSHGARGSLQOVLPLPPNSD 379
 OY 372 SREGSIENFLOFLOGTCPSSEWVSRLPSKQEPAPVDFRIPQIAEE 421
 DB 380 SWSASGGTSGQLTLQOLLGGEA--TRDPPPTATYVNFVTSQVERE 427

RESULT 10
 O9GJTO PRELIMINARY; PRT; 405 AA.
 ID O9GJTO;
 AC O9GJTO;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BETA 3 ADRENERGIC RECEPTOR.
 GN B3AR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Ovis aries beta 3 adrenergic receptor (B3AR) gene - allele F,
 RT complete cds."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL: AF314205; AAG31168.1; -
 DR EMBL: AF314201; AAG31164.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_FL2; 1.
 DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 KW SEQUENCE 405 AA; 42956 MW; 6C9F81EBAF93C578 CRC64;

Query Match 14.1%; Score 327.5; DB 6; Length 405;
 Best Local Similarity 29.4%; Pred. No. 1.4e-20;

Matches 116; Conservative 61; Mismatches 171; Indels 47; Gaps 17;

7 POSSGNSSTLGRVPTP--GPST--ASGVPEVGLRDVASESYALFFMLLDLTAVAGNAA 62
 3 PMPGNSNS-LTPWPDIPPLAPNTANASGLPGVPW---AVALAGALLALAVLATVAGNLL 57
 63 VMAVIAKTPALRK--VFVPHLCVLDLAAALTPLMLAMSSSALFDHALFGEVACRYLYF 120
 58 VYVAIARTPRLOQTMNVTSLATADLVVGLLVPPG--ATLALGHMPPLGVTCGELMTS 115
 121 LSVCSVSTALISVSAINERYVYVHPMRXEVRMTGLVASLVGVWVKALAMASVPVYG 180
 116 VDVLCTVSTIETLCALAVDRYLAVTNPLRYGALVTKRRARAIVLVWVSAVSPAPIMS 175
 181 RVSMEGAPSVPPGCSLOMSHSAYCOL-----FVVVFAVLFFLLPLLLILVYCSMPRYA 235
 176 K-WMVRVGADEAQRCH---SNPRCTFASNMRYALLSSSVSYLPLVLVLYAVAVFYVA 231
 236 ---RVAAHQGPPLPTMETPR-QRSESLSRSTVWTSAGP-----QTPPHRTFCGG 283
 232 TROLRLRLRELGRFPPESSPPAPSRSGSPAGPYASPGVSYGRARRALLPLREH--- 288
 284 KAAVLLAVGGOFLCWLPRFSFHLVYVLSAOPISGQVESVYTWIGFCTSPFFGYC 343
 289 RALRLTGLMGFTLCWLPFFVNVVNRALGSPVSGPTFLALNMLGYANSAFNPLY-C 347
 344 LNROIRGELSKQVCFKFPARPEEL-----RLPS 372
 348 RSPDFRSAP-RRLLC--RCPPPEHLAASPPRAP 379

RESULT 11

09GL56 PRELIMINARY; PRT; 405 AA.

AC 09GL56: 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA 3 ADRENERGIC RECEPTOR.
 GN B3AR.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprine; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF314203; AAG31166.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SO SEQUENCE 405 AA; 42886 MW; EF4B13BBA13EA413 CRC64;

Query Match 14.1%; Score 327.5; DB 6; Length 405;
 Best Local Similarity 29.1%; Pred. No. 1.4e-20;
 Matches 115; Conservative 62; Mismatches 171; Indels 47; Gaps 17;

7 POSSGNSSTLGRVPTP--GPST--ASGVPEVGLRDVASESYALFFMLLDLTAVAGNAA 62
 3 PMPGNSNS-LTPWPDIPPLAPNTANASGLPGVPW---AVALAGALLALAVLATVAGNLL 57
 63 VMAVIAKTPALRK--VFVPHLCVLDLAAALTPLMLAMSSSALFDHALFGEVACRYLYF 120
 58 VYVAIARTPRLOQTMNVTSLATADLVVGLLVPPG--ATLALGHMPPLGVTCGELMTS 115
 121 LSVCSVSTALISVSAINERYVYVHPMRXEVRMTGLVASLVGVWVKALAMASVPVYG 180
 116 VDVLCTVSTIETLCALAVDRYLAVTNPLRYGALVTKRRARAIVLVWVSAVSPAPIMS 175
 181 RVSMEGAPSVPPGCSLOMSHSAYCOL-----FVVVFAVLFFLLPLLLILVYCSMPRYA 235
 176 K-WMVRVGADEAQRCH---SNPRCTFASNMRYALLSSSVSYLPLVLVLYAVAVFYVA 231
 236 ---RVAAHQGPPLPTMETPR-QRSESLSRSTVWTSAGP-----QTPPHRTFCGG 283
 232 TROLRLRLRELGRFPPESSPPAPSRSGSPAGPYASPGVSYGRARRALLPLREH--- 288
 284 KAAVLLAVGGOFLCWLPRFSFHLVYVLSAOPISGQVESVYTWIGFCTSPFFGYC 343
 289 RALRLTGLMGFTLCWLPFFVNVVNRALGSPVSGPTFLALNMLGYANSAFNPLY-C 347
 344 LNROIRGELSKQVCFKFPARPEEL-----RLPS 372
 348 RSPDFRSAP-RRLLC--RCPPPEHLAASPPRAP 379

RESULT 12

09GL57 PRELIMINARY; PRT; 405 AA.

AC 09GL57: 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA 3 ADRENERGIC RECEPTOR.
 GN B3AR.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprine; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF314200; AAG31163.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SO SEQUENCE 405 AA; 42928 MW; 6C9F81EBAF90F54B CRC64;

Query Match 14.1%; Score 326.5; DB 6; Length 405;
 Best Local Similarity 29.3%; Pred. No. 1.8e-20;

Matches 114; Conservative 61; Mismatches 173; Indels 41; Gaps 16;

7 POSSGNSSTLGRVPTP--GPST--ASGVPEVGLRDVASESYALFFMLLDLTAVAGNAA 62
 3 PMPGNSNS-LTPWPDIPPLAPNTANASGLPGVPW---AVALAGALLALAVLATVAGNLL 57
 63 VMAVIAKTPALRK--VFVPHLCVLDLAAALTPLMLAMSSSALFDHALFGEVACRYLYF 120
 58 VYVAIARTPRLOQTMNVTSLATADLVVGLLVPPG--ATLALGHMPPLGVTCGELMTS 115
 121 LSVCSVSTALISVSAINERYVYVHPMRXEVRMTGLVASLVGVWVKALAMASVPVYG 180
 116 VDVLCTVSTIETLCALAVDRYLAVTNPLRYGALVTKRRARAIVLVWVSAVSPAPIMS 175
 181 RVSMEGAPSVPPGCSLOMSHSAYCOL-----FVVVFAVLFFLLPLLLILVYCSMPRYA 235
 176 K-WMVRVGADEAQRCH---SNPRCTFASNMRYALLSSSVSYLPLVLVLYAVAVFYVA 231
 236 ---RVAAHQGPPLPTMETPR-QRSESLSRSTVWTSAGP-----QTPPHRTFCGG 283
 232 TROLRLRLRELGRFPPESSPPAPSRSGSPAGPYASPGVSYGRARRALLPLREH--- 288
 284 KAAVLLAVGGOFLCWLPRFSFHLVYVLSAOPISGQVESVYTWIGFCTSPFFGYC 343
 289 RALRLTGLMGFTLCWLPFFVNVVNRALGSPVSGPTFLALNMLGYANSAFNPLY-C 347
 344 LNROIRGELSKQVCFKFPARPEEL-----RLPS 372
 348 RSPDFRSAP-RRLLC--RCPPPEHLAASPPRAP 379

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Db 58 VIVAARTPRLOTMTNVTSLATADVLGVPPG--ATLATGHPMLGTGCELWTS 115
Qy 121 LSVCFVSLAISVAINERYVYVHPMRVEVMTLGLVASVLGVWKALAMASVPLG 180
Db 116 VDVLCAVTSITETLCAVLADRLAVTNPLRGALYTKRRARAVLVWVSAVSAPLMS 175
Qy 181 RVSMEGAPSVPGCSLQMSAYCOL-----FVVFAVLVELLPILLILVYCSMPFVA 235
Db 176 K-WMRVGAADAQORCH---SNPRCCTFASNMYPALLSSVSFYLPILVMLVYARVYVA 231
Qy 236 ---RVAAHQGLPTMETPR-ORSESLSSRSTWVTSSGAP-----QTPHRTGGG 283
Db 232 TROLRLRLRELGRPPESPAPSRGSPGAPVSPVGVGRPARLLPLREH--- 288
Qy 284 KAAVVLAVAGQFLCMLPFSFHLVYALSQPISTGVESVWIGFCTSNPFEGC 343
Db 289 RALFTLGLMGTFTLCMLPFVVNVVNRALGSPSLVSGFTLALMWLGANSAPNPLTY-C 347
Qy 344 LNRQIRGELSKOFVCFKPAPEELRLPS 372
Db 348 RSPDFRSAP-RRLIC--RCPEEHLAAS 373

RESULT 13
Q9NG02 PRELIMINARY; PRT; 399 AA.
ID 09NG02:
AC 09NG02:
DT 01-OCT-2000 (Tremblrel, 15, Created)
DT 01-OCT-2000 (Tremblrel, 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN TYR1.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
OX NCBI_Taxid=7460;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20155587; PubMed=10693920;
RA Bienau W., Ballenz S., Baumann A.;
RT "myt1: characterization of a gene from honeybee (Apis mellifera)
RT brain encoding a functional tyramine receptor.";
RL J. Neurochem. 74:900-908(2000).
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ245824; CAB76374.1; -.
DR HSSP: P29274; IMM.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 399 AA; 44650 MW; F5FE4E4F1336433 CRC64;

Query Match 13.98; Score 322; DB 5; Length 399;
Best Local Similarity 23.68; Pred. No. 4.3e-20;
Matches 100; Conservative 64; Mismatches 139; Indels 88; Gaps 12;

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Db 188 -----COLTRQGVYVYSSLOSFFILPLMSLVLEITLARRRURERAROSRLNAYST 242
Qy 242 -----HGRLPTMETPRORSES--LSSRSTWVTSSGAPQTPHRTGG 282
Db 243 RHRBADAESVSSETHNE---RSTPRSHAKPSLIDDEPTEVTIGGGTSSRRRTGS 298
Qy 283 -----GKAAVVLAVAGQFLCMLPFSFHLVYALSQPISTGVESVWIGFCTSNPFEGC 343
Db 299 RAAATTTVQFIEERORISLSKERRAARTLGVMGVFWCMLPFPLVYVTPCPDCCP 358
Qy 319 TGQVESVWTVIGFCTSNPFEGCLNQR 349
Db 359 SDRMYVFTWGLGVNSALNPLTYITFNLDYR 389

RESULT 14
Q90X46 PRELIMINARY; PRT; 402 AA.
ID 090X46:
AC 090X46:
DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE SC:B22015.4 (NOVEL PROTEIN SIMILAR TO HUMAN G-PROTEIN COUPLED RECEPTOR RE2).
GN SC:B22015.4.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN 11
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL590146; CAC94897.1; -.
KW Receptor.
SQ SEQUENCE 402 AA; 44373 MW; 5FB8875874267F00 CRC64;

Query Match 13.78; Score 318.5; DB 13; Length 402;
Best Local Similarity 27.78; Pred. No. 8.8e-20;
Matches 96; Conservative 69; Mismatches 145; Indels 37; Gaps 11;

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DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE ALPHA 1-ADRENERGIC RECEPTOR SUBTYPE ALPHA 1D, ALPHA 1D-AR.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9210054; PubMed=1661838;
 RA Perez D.M., Plascik M.T., Graham R.M.;
 RT "Solution-phase library screening for the identification of rare
 RT clones: Isolation of an alpha 1D-adrenergic receptor cDNA."
 RL M01. Pharmacol. 40:876-883(1991).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 SQ SEQUENCE 559 AA; 59739 MM; 37CD9BD696D3A47D CRC64;

 Query Match 13.7% Score 316.5; DB 11; Length 559;
 Best Local Similarity 26.1% Pred. No. 1.9e-19;
 Matches 102; Conservative 76; Mismatches 156; Indels 57; Gaps 15;

 QY 6 IPQSSGNSSTL-----GRVPQT-----PGPSTA---SGVPEVGLRDVASEVAL-FFMLILD 53
 DB 42 VPGATGGGAAVGTSGGETNOSTSGECAAAGEVNSAAGLVASAGVGVGFLAFT 101
 QY 54 LTAAGNAANAIAKTPALRKVV--EVFHLCLVDLLAALTMLPLMLSSALFDHALFG 111
 DB 102 LTAAGNLVLIVSAACNRHLQTVNYFIVNLAVADLLSAVALPPS--ATMEVLGFMAFG 159
 QY 112 EVACRLVLEFVSCFVSLAIVSAINERYYYVHPMYEVKMTLGLVASLVGVWAKAL 171
 DB 160 RTFCDVMAAVDVLCTASISLCTISVDRYGVGRHSLSKYPAIMIERKAAAILALMAVAL 219
 QY 172 AMAVVPVIGRVSMEGASVSPGCSLQWSHSAAYOL-----FVYFAVLVFLPLLLILV 226
 DB 220 VASVGPLG---MKE---VPP-----DERFCGITEEVGAIIPSSVCSFYLLPMAVIV 266
 QY 227 VYCSMFVYAR--VAMQHGPLPTWMEYTPROKSE--SLSSRSITWYSSGAP--QTPPHRT 279
 DB 267 MYCAVYVVARSTTSLEAG---IKREPKASEVVLRIHCRGARTSAKGYPTQSSKGT 322
 QY 280 FGGC-----KAAYVLLAVGGOFLLCWLPEYFSLHYVALSAQPISTGOVESVYT 327
 DB 323 LRSSLVRLLEKFSREKKAAKTLAIYGVFLCWPEFFFLPLGSIPIKPSGCVFKYIF 382
 QY 328 WIGYFCFTSNPFYGCINROI RGLSKQFVC 358
 DB 383 WLGTFNSCVNPLIYPCSSREKRAFLRLRC 413

Search completed: October 21, 2002, 16:10:47
 Job time : 37 secs